

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: November 9, 2002, 19:42:10 ; Search time 12895 Seconds  
(without alignments)  
11808.133 Million cell updates/sec  
Title: US-09-974-592-3  
Perfect score: 5232  
Sequence: 1 gaaaggtgacagtccta.....tcaaaaaaaaaaaaaaaag 5232  
Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0  
Searched: 2054640 seqs, 14551402878 residues  
Word size : 0  
Total number of hits satisfying chosen parameters: 4109280  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Listing first 45 summaries

Database : GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_cm.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*  
15: em\_ba.\*  
16: em\_fun.\*  
17: em\_hum.\*  
18: em\_in.\*  
19: em\_mu.\*  
20: em\_om.\*  
21: em\_or.\*  
22: em\_ov.\*  
23: em\_pat.\*  
24: em\_ph.\*  
25: em\_pl.\*  
26: em\_ro.\*  
27: em\_sts.\*  
28: em\_un.\*  
29: em\_vi.\*  
30: em\_htg\_hum.\*  
31: em\_htg\_inv.\*  
32: em\_htg\_other.\*  
33: em\_htg\_mus.\*  
34: em\_htg\_pln.\*  
35: em\_htg\_rnd.\*  
36: em\_htg\_man.\*  
37: em\_htg\_vrt.\*  
38: em\_sy.\*  
39: em\_htgo\_hum.\*  
40: em\_htgo\_mus.\*  
41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	5232	100.0	5232	6	AR106397	AR106397 Sequence
2	5232	100.0	5232	6	AR116699	AR116699 Sequence
3	3523	67.3	123742	2	HS167P19	Z93014 Homo sapien
4	3523	67.3	133391	9	HS0315G1	AL121601 Human DNA
5	3523	67.3	201197	2	HS424J12	Z82207 Homo sapien
6	2278	43.5	3000	6	AX412131	AX412131 Sequence
7	2027	38.7	2404	6	AX429575	AX429575 Sequence
8	1990	38.0	2540	6	AR103281	AR103281 Sequence
9	1990	38.0	2540	6	AX412118	AX412118 Sequence
10	1990	38.0	2540	6	HSU45880	U45880 Human X-lin
11	1757	33.6	2086	9	BC032729	BC032729 Homo sapi
12	1560	29.8	1659	6	E31042	E31042 Method for
13	1560	29.8	1659	9	HSU32974	U32974 Human IAP-1
14	912	17.4	201197	2	HS424J12	Z82207 Homo sapien
15	146	2.8	158093	9	AL390123	AL390123 Human DNA
16	128	2.4	185771	2	AC111718	AC111718 Rattus no
17	114	2.2	158075	2	AC131311	AC131311 Homo sapi
18	112	2.1	69937	2	AC069566	AC069566 Homo sapi
19	112	2.1	150107	2	AC027582	AC027582 Homo sapi
20	112	2.1	184406	9	AC009476	AC009476 Homo sapi
21	112	2.1	313264	2	AC023053	AC023053 Homo sapi
22	108	2.1	147598	9	AC093503	AC093503 Homo sapi
23	108	2.1	173316	2	AC025983	AC025983 Homo sapi
24	107	2.0	112902	9	AC005230	AC005230 Homo sapi
25	107	2.0	145556	2	CNS07EEU	AL445903 Human chr
26	107	2.0	160653	2	AC026306	AC026306 Homo sapi
27	106	2.0	161381	2	AC120024	AC120024 Homo sapi
28	103	2.0	40271	2	AC090411	AC090411 Homo sapi
29	103	2.0	40328	9	HSAC000021	AC000021 Origins o
30	103	2.0	43795	9	AC000022	AC000022 Genomic s
31	103	2.0	85674	9	AF164343	AF164343 Homo sapi
32	103	2.0	103356	9	AC010089	AC010089 Homo sapi
33	103	2.0	141580	9	AF241729	AF241729 Homo sapi
34	103	2.0	163494	2	AC016964	AC016964 Homo sapi
35	103	2.0	166937	9	AC025679	AC025679 Homo sapi
36	103	2.0	171987	9	AC100757	AC100757 Homo sapi
37	103	2.0	177355	9	AC023310	AC023310 Homo sapi
38	103	2.0	180345	9	AC006983	AC006983 Homo sapi
39	103	2.0	184637	2	AC006990	AC006990 Homo sapi
40	103	2.0	186838	9	AC006338	AC006338 Homo sapi
41	103	2.0	187313	9	AC022212	AC022212 Homo sapi
42	103	2.0	190506	2	AC068990	AC068990 Homo sapi
43	103	2.0	199458	9	AC010088	AC010088 Homo sapi
44	103	2.0	207471	2	AP001401	AP001401 Homo sapi
45	102	1.9	63966	9	AL451141	AL451141 Human DNA

ALIGNMENTS

RESULT 1  
AR106397  
LOCUS  
DEFINITION Sequence 3 from patent US 6107041.  
ACCESSION AR106397  
VERSION AR106397.1 GI:12820927  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5232)  
AUTHORS Korneluk,R.G., MacKenzie,A.E., Liston,P., Baird,S., Tsang,B.K. and Pratt,C.  
TITLE Detection and modulation of IAPs for the diagnosis and treatment of proliferative disease

AR106397 5232 bp DNA linear PAT 14-FEB-2001

JOURNAL Patent: US 6107041-A 3 22-AUG-2000;

FEATURES Location/Qualifiers

source 1. 5232

BASE COUNT 1579 a 861 c 1062 g 1728 t 2 others

ORIGIN

Query Match 100.0%; Score 5232; DB 6; Length 5232;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 5232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAAGGTGGACAGTCTCTATTTTCAAGAGAGATGACTTTTAAACAGTTTGAAGGATCT 60  
Db 1 GAAAGGTGGACAGTCTCTATTTTCAAGAGAGATGACTTTTAAACAGTTTGAAGGATCT 60  
Qy 61 AAAACCTTGTGTACCTGCAGACATCAATTAAGGAAGAAATTTGTAGAAGAGTTTAATAGA 120  
Db 61 AAAACCTTGTGTACCTGCAGACATCAATTAAGGAAGAAATTTGTAGAAGAGTTTAATAGA 120  
Qy 121 TTAATAAATCTTTTGCCTTAATTTTCCAAAGTGGTAGTCTCTGTTTCAGCATCAACACTGGCAGGA 180  
Db 121 TTAATAAATCTTTTGCCTTAATTTTCCAAAGTGGTAGTCTCTGTTTCAGCATCAACACTGGCAGGA 180  
Qy 181 GCAGGGTTTCTTTATACCTGTGAAGGAGATACCGTGCCTGTTTGTAGTTCATGCACT 240  
Db 181 GCAGGGTTTCTTTATACCTGTGAAGGAGATACCGTGCCTGTTTGTAGTTCATGCACT 240  
Qy 241 GTAGATAGATGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAAGTATCCCAAAAT 300  
Db 241 GTAGATAGATGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAAGTATCCCAAAAT 300  
Qy 301 TGCAGATTTATCAAGCGCTTTTATCTTGAATAATAGTGCAGCAGCTACAAAATCTCGT 360  
Db 301 TGCAGATTTATCAAGCGCTTTTATCTTGAATAATAGTGCAGCAGCTACAAAATCTCGT 360  
Qy 361 ATCCAGATGTCAGTACAAAGTTGAAACTATCTGGAAGACAGAGATCAATTTGCCCTTA 420  
Db 361 ATCCAGATGTCAGTACAAAGTTGAAACTATCTGGAAGACAGAGATCAATTTGCCCTTA 420  
Qy 421 GACAGGCATCTGACACATGCGACATCTCTTTTGAAGTGGCAGCTGTAGATATA 480  
Db 421 GACAGGCATCTGACACATGCGACATCTCTTTTGAAGTGGCAGCTGTAGATATA 480  
Qy 481 TCAGACACCATATACCCGAGGAACCTGCCATGTATAGTGAAGAGCTAGATTTAAAGTCC 540  
Db 481 TCAGACACCATATACCCGAGGAACCTGCCATGTATAGTGAAGAGCTAGATTTAAAGTCC 540  
Qy 541 TTTGAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGATTTAGCAAGTCTGGACTC 600  
Db 541 TTTGAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGATTTAGCAAGTCTGGACTC 600  
Qy 601 TACTACACAGGTATTGGTGACCAAGTGCAGTCTTTTGTGGTGGAAAACCTGAAAAT 660  
Db 601 TACTACACAGGTATTGGTGACCAAGTGCAGTCTTTTGTGGTGGAAAACCTGAAAAT 660  
Qy 661 TGGGAACCTTGTGATCGTGGTGCAGACACAGCGACACTTTCCCTAAATGCTCTTT 720  
Db 661 TGGGAACCTTGTGATCGTGGTGCAGACACAGCGACACTTTCCCTAAATGCTCTTT 720  
Qy 721 GTTTTGGCCCGGAATCTTAATATTGGAAGTGAATCTGATGCTGTGATAGGAAT 780  
Db 721 GTTTTGGCCCGGAATCTTAATATTGGAAGTGAATCTGATGCTGTGATAGGAAT 780  
Qy 781 TTCCCAAAATTCACAAATCTTCCAAAGAAATCCATCCATGGCAGATTAAGACACGGATC 840  
Db 781 TTCCCAAAATTCACAAATCTTCCAAAGAAATCCATCCATGGCAGATTAAGACACGGATC 840  
Qy 841 TTTACTTTTGGGACATGGATATCTACGTAAACAGGAGCAGCTTGCAGAGCTGGATTT 900  
Db 841 TTTACTTTTGGGACATGGATATCTACGTAAACAGGAGCAGCTTGCAGAGCTGGATTT 900  
Qy 901 TATGCTTAGGTGAAGGTGATAAAGTAAAGTCTTCTACTGTGGAGGAGGCTAACTGAT 960  
Db 901 TATGCTTAGGTGAAGGTGATAAAGTAAAGTCTTCTACTGTGGAGGAGGCTAACTGAT 960

Db 901 TATGCTTTAGTGAAGGTGATAAAGTAAAGTCTTCTACTGTGGAGGAGGCTAACTGAT 960  
Qy 961 TGGAGGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCAAATAT 1020  
Db 961 TGGAGGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCAAATAT 1020  
Qy 1021 CTGTTTAGAACAGAGGAGCAAGAATATATAACAATATTTCAATTTAACTCACTTCACTTGAG 1080  
Db 1021 CTGTTTAGAACAGAGGAGCAAGAATATATAACAATATTTCAATTTAACTCACTTCACTTGAG 1080  
Qy 1081 GAGTGTCTGGTGAAGAACTACTGAGAAAACACCATCACTAACTAGAGAATTTGATGATACC 1140  
Db 1081 GAGTGTCTGGTGAAGAACTACTGAGAAAACACCATCACTAACTAGAGAATTTGATGATACC 1140  
Qy 1141 ATCTTCCAAAATCCCTATGCTACAAAGAACTATACCAATGGGGTTCAGTTTCAAGGACATT 1200  
Db 1141 ATCTTCCAAAATCCCTATGCTACAAAGAACTATACCAATGGGGTTCAGTTTCAAGGACATT 1200  
Qy 1201 AAGAAAATTAATGGAGGAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTGAAGTT 1260  
Db 1201 AAGAAAATTAATGGAGGAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTGAAGTT 1260  
Qy 1261 CTGTTGAGATCTAGTGAATGCTCAGAAAACAGATATGCAAGATGAGTCAAGTCACT 1320  
Db 1261 CTGTTGAGATCTAGTGAATGCTCAGAAAACAGATATGCAAGATGAGTCAAGTCACT 1320  
Qy 1321 TCATTACAGAAAGAGATTAGTACTGAAGAGCAGCTAAGGCGCTGCAAGAGGAGAGCTT 1380  
Db 1321 TCATTACAGAAAGAGATTAGTACTGAAGAGCAGCTAAGGCGCTGCAAGAGGAGAGCTT 1380  
Qy 1381 TGCAAAATCTGTATGGATAGAAATATTCGTATCTGTTTGTCTTCTTGTGGACATCTAGTC 1440  
Db 1381 TGCAAAATCTGTATGGATAGAAATATTCGTATCTGTTTGTCTTCTTGTGGACATCTAGTC 1440  
Qy 1441 ACTTGTAAACAAATGCTGCAAGCAGTTGACAAAGTGCCTCAAGTGTGACAGTCACTACT 1500  
Db 1441 ACTTGTAAACAAATGCTGCAAGCAGTTGACAAAGTGCCTCAAGTGTGACAGTCACTACT 1500  
Qy 1501 TTCAAGCAAAAATTTTATGCTTAACTTAATCTAGTAGGAGCTGTATGTTGTTCT 1560  
Db 1501 TTCAAGCAAAAATTTTATGCTTAACTTAATCTAGTAGGAGCTGTATGTTGTTCT 1560  
Qy 1561 TATTACCCCTGATTTGAATGTGTGATGTAAGTGAACCTTAAAGTAAATCAGGATTTCAAT 1620  
Db 1561 TATTACCCCTGATTTGAATGTGTGATGTAAGTGAACCTTAAAGTAAATCAGGATTTCAAT 1620  
Qy 1621 TAGCAATTTGCTACCAAGTAGGAAAAAATGTACATGCGAGTGTAGTTGGCAATATA 1680  
Db 1621 TAGCAATTTGCTACCAAGTAGGAAAAAATGTACATGCGAGTGTAGTTGGCAATATA 1680  
Qy 1681 ATCTTTGAATTTCTTGAATTTTCAGGGTATTAGCTGTATATCCATTTTTTACTGTTA 1740  
Db 1681 ATCTTTGAATTTCTTGAATTTTCAGGGTATTAGCTGTATATCCATTTTTTACTGTTA 1740  
Qy 1741 TTTAATTTGAAACCATAGACTAAGAATAAGAAAGCATCACTATAACTGAACAAATGTT 1800  
Db 1741 TTTAATTTGAAACCATAGACTAAGAATAAGAAAGCATCACTATAACTGAACAAATGTT 1800  
Qy 1801 ATTCATAGTACTGATTTAATTTCTAAGTGAATTAATCACTCTGGATTTTTAT 1860  
Db 1801 ATTCATAGTACTGATTTAATTTCTAAGTGAATTAATCACTCTGGATTTTTAT 1860  
Qy 1861 TCTTTTCAGATAGGCTTAACAAATGGAGCTTCTGTATATAAATGTGAGATTTAGAGTTA 1920  
Db 1861 TCTTTTCAGATAGGCTTAACAAATGGAGCTTCTGTATATAAATGTGAGATTTAGAGTTA 1920  
Qy 1921 ATCTCCCAATCACATAATTTGTTTGTGAAAAAGGAATAAATGTTCCATGCTGTTG 1980  
Db 1921 ATCTCCCAATCACATAATTTGTTTGTGAAAAAGGAATAAATGTTCCATGCTGTTG 1980  
Qy 1981 GAAAGATAGAGATTTGTTTGTAGAGGTTGGTGTGTTTGTAGGATTTCTGTCATTTCT 2040  
Db 1981 GAAAGATAGAGATTTGTTTGTAGAGGTTGGTGTGTTTGTAGGATTTCTGTCATTTCT 2040

QY 2041 TTTAAAGTTATAAACACGTACTTGTGCGAATATATTTTTTAAAGTGATTTGCCATTTTGG 2100  
DB TTTAAAGTTATAAACACGTACTTGTGCGAATATATTTTTTAAAGTGATTTGCCATTTTGG 2100  
QY 2101 AAAGCGTATTTAATGATPAGAAATACTATPCAGGCCAACATGACTGACATGGAAGAATCTCA 2160  
DB AAAGCGTATTTAATGATPAGAAATACTATPCAGGCCAACATGACTGACATGGAAGAATCTCA 2160  
QY 2161 AAGATATGTTAAAGTAAATGCAAGTGGCAAAACACTATGATCTGAGCCAGATCA 2220  
DB AAGATATGTTAAAGTAAATGCAAGTGGCAAAACACTATGATCTGAGCCAGATCA 2220  
QY 2221 AAGTATGATGTTTTTAAATATGATAGCAACAAAAGATTTGGAAAGATATACACCAAACTG 2280  
DB AAGTATGATGTTTTTAAATATGATAGCAACAAAAGATTTGGAAAGATATACACCAAACTG 2280  
QY 2281 TTAATGCTGTTCTCTTCGCGGAGGGGGGATTTGGGGAGGGGCCCCAGAGGGGTTTTA 2340  
DB TTAATGCTGTTCTCTTCGCGGAGGGGGGATTTGGGGAGGGGCCCCAGAGGGGTTTTA 2340  
QY 2341 TAGGGGCTTTTACATTTCTACTTTTTCATTTTGTCTGTCGAAATTTTATAAGTAT 2400  
DB TAGGGGCTTTTACATTTCTACTTTTTCATTTTGTCTGTCGAAATTTTATAAGTAT 2400  
QY 2401 GTATTACTTTTGAATCAGAAATTTTGAAGATATTTTGTCTGTCGAAATTTTATAAGTAT 2460  
DB GTATTACTTTTGAATCAGAAATTTTGAAGATATTTTGTCTGTCGAAATTTTATAAGTAT 2460  
QY 2461 GTTCAACGCCGCGAAACACTATACACTCAGCTGTTAGTTTTTCTAATCCAAAGAAGCA 2520  
DB GTTCAACGCCGCGAAACACTATACACTCAGCTGTTAGTTTTTCTAATCCAAAGAAGCA 2520  
QY 2521 GGCAGTTAACCTTTTGTGGCAATCTGAAATGTAATGTAATGTTATGTTTTTCTCTGCT 2580  
DB GGCAGTTAACCTTTTGTGGCAATCTGAAATGTAATGTAATGTTATGTTTTTCTCTGCT 2580  
QY 2581 TGTGGATGAAAAATATTTCTGAGTGGTAGTTTTTGTACAGGTAGACCATGCTTTATCTTG 2640  
DB TGTGGATGAAAAATATTTCTGAGTGGTAGTTTTTGTACAGGTAGACCATGCTTTATCTTG 2640  
QY 2641 TTTCAAAATAGTATTTCTGATTTTGTAAATGAAATATATAATATGCTCAGACTCTCC 2700  
DB TTTCAAAATAGTATTTCTGATTTTGTAAATGAAATATATAATATGCTCAGACTCTCC 2700  
QY 2701 AATTAATGATGAGTATTCATCTTAATCTGCTAGCTTTAAGCCTGCCTAAGCTCACTTT 2760  
DB AATTAATGATGAGTATTCATCTTAATCTGCTAGCTTTAAGCCTGCCTAAGCTCACTTT 2760  
QY 2761 ACTAAAAAGATCTTTGTTAACTCAGTATTTTAAACATCTGTCAGCTTATGTAGGTAAAAAGT 2820  
DB ACTAAAAAGATCTTTGTTAACTCAGTATTTTAAACATCTGTCAGCTTATGTAGGTAAAAAGT 2820  
QY 2821 AGAAGCATGTTGTACACTGCTGTAGTTATAGTGACAGCTTTCCATGTTGAGATTCCTCA 2880  
DB AGAAGCATGTTGTACACTGCTGTAGTTATAGTGACAGCTTTCCATGTTGAGATTCCTCA 2880  
QY 2881 TATCATCTGTAATCTTAAAGTTTCACTGAGTTTTTACCGTTAGGATGATTAAGATCTAT 2940  
DB TATCATCTGTAATCTTAAAGTTTCACTGAGTTTTTACCGTTAGGATGATTAAGATCTAT 2940  
QY 2941 ATAGGCAAAAATGTTAAAGTCTTCTCCTACATTTGTTTTCTGGCTAGTAAATAGTA 3000  
DB ATAGGCAAAAATGTTAAAGTCTTCTCCTACATTTGTTTTCTGGCTAGTAAATAGTA 3000  
QY 3001 GTAGATCTTCTGAAATAAATGTTCTCCTCAAGATCCCTTAAACCTCTGGAATATATAA 3060  
DB GTAGATCTTCTGAAATAAATGTTCTCCTCAAGATCCCTTAAACCTCTGGAATATATAA 3060  
QY 3061 AATATTGCGAAGAAAGAAAGTGTGTTTAAATATTTTTTAAAAAACACTTGAATAAG 3120  
DB AATATTGCGAAGAAAGAAAGTGTGTTTAAATATTTTTTAAAAAACACTTGAATAAG 3120

QY 3121 AATCAGTAGGTATAAACTAGAACTTTAAAAATGCCATAGAACGCTCCAGGGTTTACAT 3180  
DB AATCAGTAGGTATAAACTAGAACTTTAAAAATGCCATAGAACGCTCCAGGGTTTACAT 3180  
QY 3181 TACAAGATTTCTACAACAACCCCATTTGTAGAGGTGAGTAAAGCATGTTTACTACAGAGAA 3240  
DB TACAAGATTTCTACAACAACCCCATTTGTAGAGGTGAGTAAAGCATGTTTACTACAGAGAA 3240  
QY 3241 AGTTTGAGAGTAAACCTGTAATAAATATATTTTTTGTGTTACTTTCTAAAGAGAAGACTA 3300  
DB AGTTTGAGAGTAAACCTGTAATAAATATATTTTTTGTGTTACTTTCTAAAGAGAAGACTA 3300  
QY 3301 TTGTTATGTTCTCTCTAACTTTCTGTTGATTTACTACTTTAAAGTATATTCATTTAAACATT 3360  
DB TTGTTATGTTCTCTCTAACTTTCTGTTGATTTACTACTTTAAAGTATATTCATTTAAACATT 3360  
QY 3361 GCAAAATTTATTTATTTATTTATTTTCTTTTTCAGATGGAGTCTTGTCTCAGCCAGG 3420  
DB GCAAAATTTATTTATTTATTTATTTTCTTTTTCAGATGGAGTCTTGTCTCAGCCAGG 3420  
QY 3421 CTGGAGTGCAGTGGAGTGATCTCTGCTCAGTCAACCTCCGCCCTTCTGGGTTCAAGCGAT 3480  
DB CTGGAGTGCAGTGGAGTGATCTCTGCTCAGTCAACCTCCGCCCTTCTGGGTTCAAGCGAT 3480  
QY 3481 TCTCGTCCCTCAGCTTCTCTGAGTAGCTGGAAATACAGCAGGTGCCACCATGCCGACTA 3540  
DB TCTCGTCCCTCAGCTTCTCTGAGTAGCTGGAAATACAGCAGGTGCCACCATGCCGACTA 3540  
QY 3541 ATTTTTTTTTTATTTTTAGTAGAGAGGGGTTTACCATGTTGGCCAGGCTGGTATCAAAAC 3600  
DB ATTTTTTTTTTATTTTTAGTAGAGAGGGGTTTACCATGTTGGCCAGGCTGGTATCAAAAC 3600  
QY 3601 TCCGTGACCTCAAGAGATCCACTCGCTTGCCTCCCAAGTCTGGGATTAACAGCTTGA 3660  
DB TCCGTGACCTCAAGAGATCCACTCGCTTGCCTCCCAAGTCTGGGATTAACAGCTTGA 3660  
QY 3661 GCCACACGCCCGGCTAAAACATTTGCAAAATTTAAATGAGAGTTTTAAAAATTAATG 3720  
DB GCCACACGCCCGGCTAAAACATTTGCAAAATTTAAATGAGAGTTTTAAAAATTAATG 3720  
QY 3721 ACTGCCCTGTTTCTGTTTATGATGTAATCTCAGTCTTTCACCTTTGCAGCTGCTGCC 3780  
DB ACTGCCCTGTTTCTGTTTATGATGTAATCTCAGTCTTTCACCTTTGCAGCTGCTGCC 3780  
QY 3781 ACTTAGTTTGGTTATATAGTCATTAACCTGTAATTTGGTCTGTATAGCTAGACTTTAAAT 3840  
DB ACTTAGTTTGGTTATATAGTCATTAACCTGTAATTTGGTCTGTATAGCTAGACTTTAAAT 3840  
QY 3841 TTAAGTTTTTCTACAAGGGGAGAAAAGTGTAAAAATTTTTTAAAAATATGTTTTCCAGGACA 3900  
DB TTAAGTTTTTCTACAAGGGGAGAAAAGTGTAAAAATTTTTTAAAAATATGTTTTCCAGGACA 3900  
QY 3901 CTTTCACCTTCCAAGTCAGGTAGGTAGTTCAATCTAGTTGTTAGCCCAAGGACTCAAGGACTG 3960  
DB CTTTCACCTTCCAAGTCAGGTAGGTAGTTCAATCTAGTTGTTAGCCCAAGGACTCAAGGACTG 3960  
QY 3961 AATTTGTTTTTAAACATAAGCTTTTCTGTTCTGGAGCGGCACTTCAATTTAAATTTCTCTCA 4020  
DB AATTTGTTTTTAAACATAAGCTTTTCTGTTCTGGAGCGGCACTTCAATTTAAATTTCTCTCA 4020  
QY 4021 AAACCTGTATGTTTATAGAGTTAAAGCAAGACTTTTTTCTCTCTCCATGAGTTGTAAT 4080  
DB AAACCTGTATGTTTATAGAGTTAAAGCAAGACTTTTTTCTCTCTCCATGAGTTGTAAT 4080  
QY 4081 TTAATGACAAACGCTGATGGCTTAAACAGTTTATTTTAAAGATTTTGTAGAAATGCTGT 4140  
DB TTAATGACAAACGCTGATGGCTTAAACAGTTTATTTTAAAGATTTTGTAGAAATGCTGT 4140  
QY 4141 TGCTTCAGGTTCTTAAATCACTCAGCACTCCAACTTCTTAATCAATTTTTTTGGAGACTTA 4200  
DB TGCTTCAGGTTCTTAAATCACTCAGCACTCCAACTTCTTAATCAATTTTTTTGGAGACTTA 4200  
QY 4201 ACAGCATTTGTTCTGTTGTTGAACATATAAAAAAGCACCGGATCTTTTCCATCTAAATCCGCA 4260

||||| 4201 ACAGATTGCTGTGTTGAACATATAAAAGCACCGGATCTTTTCCATCTAATTTCCGCA 4260  
Qy 4261 AAAATTGATCATTTGCAAGCAAAATATAGCCATATCCAAATCTTTTCCCTCCCAA 4320  
Db 4261 AAAATTGATCATTTGCAAGCAAAATATAGCCATATCCAAATCTTTTCCCTCCCAA 4320  
Qy 4321 GAGTTCAGTGCTACATGAGACTATTCCTTTCTGTATATAAAGTCACCTAGGATTT 4380  
Db 4321 GAGTTCAGTGCTACATGAGACTATTCCTTTCTGTATATAAAGTCACCTAGGATTT 4380  
Qy 4381 CAAGTCACCACTATTTTACATTTAGTCATGCAAGAGATTCAGTAGTTCATTAAGT 4440  
Db 4381 CAAGTCACCACTATTTTACATTTAGTCATGCAAGAGATTCAGTAGTTCATTAAGT 4440  
Qy 4441 ACTTATCTTTATTTGTAATAATTTAGTCTGCTGATCAAAAGCATTTCTTAATTTTGAG 4500  
Db 4441 ACTTATCTTTATTTGTAATAATTTAGTCTGCTGATCAAAAGCATTTCTTAATTTTGAG 4500  
Qy 4501 AACTGGTTTTAGCATTTTACAACTAAATTCAGTTAATTAATAGCTTTTATTTGCC 4560  
Db 4501 AACTGGTTTTAGCATTTTACAACTAAATTCAGTTAATTAATAGCTTTTATTTGCC 4560  
Qy 4561 TTTCTGTACATTTGGTTTTTCCCTGTCCCTTTGATTTACGGCTTAAGGTAAAG 4620  
Db 4561 TTTCTGTACATTTGGTTTTTCCCTGTCCCTTTGATTTACGGCTTAAGGTAAAG 4620  
Qy 4621 ANNGGCTAGTGAGTGATATAATGTCATTTGGCCCTGTCTATTATCATATTTTGTAT 4680  
Db 4621 ANNGGCTAGTGAGTGATATAATGTCATTTGGCCCTGTCTATTATCATATTTTGTAT 4680  
Qy 4681 TTTTGTCTTATATTTACATTTTCAGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4740  
Db 4681 TTTTGTCTTATATTTACATTTTCAGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4740  
Qy 4741 AAATTTGTATTTGAACATATGAATGGAGACTACGGCCCAAGCATTTAGTTTCATGATA 4800  
Db 4741 AAATTTGTATTTGAACATATGAATGGAGACTACGGCCCAAGCATTTAGTTTCATGATA 4800  
Qy 4801 TACCCCTTTAAACCCGAATCATTTGTTTATTTCCCTGATTACACAGGTGTGAATGGGAAA 4860  
Db 4801 TACCCCTTTAAACCCGAATCATTTGTTTATTTCCCTGATTACACAGGTGTGAATGGGAAA 4860  
Qy 4861 GGGGCTAGTATATCAGTAGGATATACTATGGGATGTATATATATATATATATATATATAT 4920  
Db 4861 GGGGCTAGTATATCAGTAGGATATACTATGGGATGTATATATATATATATATATATATAT 4920  
Qy 4921 ATGAATAAAATGGGCTGGGCTCAGTGGCTCAGCCCTGTAAATCCAGCCTTTGGGAGG 4980  
Db 4921 ATGAATAAAATGGGCTGGGCTCAGTGGCTCAGCCCTGTAAATCCAGCCTTTGGGAGG 4980  
Qy 4981 CTGAGGAGGTGGATCAGGAGTCAAGAGATCGAGACCATCTGGCTAACACGGTGAAC 5040  
Db 4981 CTGAGGAGGTGGATCAGGAGTCAAGAGATCGAGACCATCTGGCTAACACGGTGAAC 5040  
Qy 5041 CCCGCTCTACTAAAAACAGAAAATTTAGCCGGCGTGGTGGCGGCGCTGTAGTCCCA 5100  
Db 5041 CCCGCTCTACTAAAAACAGAAAATTTAGCCGGCGTGGTGGCGGCGCTGTAGTCCCA 5100  
Qy 5101 GCTACTCGGAGGCTGAGGAGGAGAAATGGTGTGNAACCCGGGAGCAGCTTGCAGTGA 5160  
Db 5101 GCTACTCGGAGGCTGAGGAGGAGAAATGGTGTGNAACCCGGGAGCAGCTTGCAGTGA 5160  
Qy 5161 GCCGAGATCTCGCCACTGCATCTCAGCTCCAGCTGGGCAACAGAGCAAGACTGTGTCTCAAAAA 5220  
Db 5161 GCCGAGATCTCGCCACTGCATCTCAGCTCCAGCTGGGCAACAGAGCAAGACTGTGTCTCAAAAA 5220  
Qy 5221 AAAAAAAG 5232  
Db 5221 AAAAAAAG 5232

RESULT 2

ARL16699 LOCUS ARL16699 5232 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 3 from patent US 6133437.  
ACCESSION ARL16699  
VERSION ARL16699.1 GI:14097021  
KEYWORDS  
SOURCE unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5232)  
AUTHORS Korneluk,R.G., MacKenzie,A.E., Liston,P., Baird,S., Tsang,B.K. and Pratt,C.  
TITLE Modulation of IAPs for the treatment of proliferative diseases  
JOURNAL Patent: US 6133437-A 3 17-OCT-2000;  
FEATURES Location/Qualifiers  
source 1..5232  
BASE COUNT 1579 a 861 c 1062 g 1728 t 2 others  
ORIGIN  
Query Match 100.0%; Score 5232; DB 6; Length 5232;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAAAGGTGGACAAGTCTCTATTTTCAAGAGAAGATGACTTTTAACAGTTTGAAGGATCT 60  
Db 1 GAAAGGTGGACAAGTCTCTATTTTCAAGAGAAGATGACTTTTAACAGTTTGAAGGATCT 60  
Qy 61 AAAACTTGTGTACCTGTCAGACATCAATAAGGAAGAAATTTGTAGAGAGTTTAATAGA 120  
Db 61 AAAACTTGTGTACCTGTCAGACATCAATAAGGAAGAAATTTGTAGAGAGTTTAATAGA 120  
Qy 121 TTAATAAATCTTTTGTCTTAATTTTCCAAGTGTAGTCTCTTTTCCAGCATCAACTGGCACA 180  
Db 121 TTAATAAATCTTTTGTCTTAATTTTCCAAGTGTAGTCTCTTTTCCAGCATCAACTGGCACA 180  
Qy 181 CGAGGTTTCTTTTATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 240  
Db 181 CGAGGTTTCTTTTATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 240  
Qy 241 GTAGATAGATGGCAATATGGAGACTTCAGCAGTTGGAAGACACAGAGAAAGTATCCCAAT 300  
Db 241 GTAGATAGATGGCAATATGGAGACTTCAGCAGTTGGAAGACACAGAGAAAGTATCCCAAT 300  
Qy 301 TGCAGATTTATCAACGGCTTTTATCTTGAAATAGTGCAGCAGCTTACAAATTTCTGGT 360  
Db 301 TGCAGATTTATCAACGGCTTTTATCTTGAAATAGTGCAGCAGCTTACAAATTTCTGGT 360  
Qy 361 ATCCAGAAATGGTCTAGTACAAAGTTGAAACTATCTGGGAAGCAGAGATCATTTGCCCTTA 420  
Db 361 ATCCAGAAATGGTCTAGTACAAAGTTGAAACTATCTGGGAAGCAGAGATCATTTGCCCTTA 420  
Qy 421 GACAGCCATCTGAGACACATGCAGACTATCTTTTGAACCTGGSCAGTGTAGATATA 480  
Db 421 GACAGCCATCTGAGACACATGCAGACTATCTTTTGAACCTGGSCAGTGTAGATATA 480  
Qy 481 TCAGACACATATACCCGAGGAACCTGCCATGTATAGTGAAGAGCTAGATTAAAGTCC 540  
Db 481 TCAGACACATATACCCGAGGAACCTGCCATGTATAGTGAAGAGCTAGATTAAAGTCC 540  
Qy 541 TTTCAGAACTGGCAGACTATGCTACCTAACCCCAAGAGAGTTAGCAAGTCTGGGACTC 600  
Db 541 TTTCAGAACTGGCAGACTATGCTACCTAACCCCAAGAGAGTTAGCAAGTCTGGGACTC 600  
Qy 601 TACTACACAGCTATTGGTGACCAAGTGCAGTCTTTTCTGTGGTGGAAAACTGAAAAAT 660  
Db 601 TACTACACAGCTATTGGTGACCAAGTGCAGTCTTTTCTGTGGTGGAAAACTGAAAAAT 660  
Qy 661 TGGGAACCTTGTGATCGTGCCTGTCAGAACACAGCGGCACACTTTTCCCTTAATTTGCTTTT 720  
Db 661 TGGGAACCTTGTGATCGTGCCTGTCAGAACACAGCGGCACACTTTTCCCTTAATTTGCTTTT 720  
Qy 721 GTTTTGGCCCGGAATCTTAATATTTCGAAGTGAATCTGATGCTGTGATGAGGAAT 780



|||||  
721 GTTTGGCGGAATCTTAATATCGAAGTGAATCTGTGCTGTGATGAAT 780  
|||||  
781 TTCCCAAAATCAACAATCTTCCAGAAATCCATCATGSCAGATTATGAACACCGATC 840  
|||||  
781 TTCCCAAAATCAACAATCTTCCAGAAATCCATCATGSCAGATTATGAACACCGATC 840  
|||||  
841 TTTACTTTTGGGACATGATATACCTCAGTTAAACAAGGAGCAGCTTCAAGAGCTGGATT 900  
|||||  
841 TTTACTTTTGGGACATGATATACCTCAGTTAAACAAGGAGCAGCTTCAAGAGCTGGATT 900  
|||||  
901 TATGCTTTTAGTGAAGGTGATAAAGTAAAGTGTCTTTCACTGTGGAGGAGGCTTAACATGAT 960  
|||||  
901 TATGCTTTTAGTGAAGGTGATAAAGTAAAGTGTCTTTCACTGTGGAGGAGGCTTAACATGAT 960  
|||||  
961 TGGAAAGCCAGTCAACACCTTGGGAACAACATGCTAAATGTTATCGACGGTGCATATAT 1020  
|||||  
961 TGGAAAGCCAGTCAACACCTTGGGAACAACATGCTAAATGTTATCGACGGTGCATATAT 1020  
|||||  
1021 CTGTTAGAACAAGGAGCAAGAATATATAACAATATTCACTTAACCTCATTCACTTTGAG 1080  
|||||  
1021 CTGTTAGAACAAGGAGCAAGAATATATAACAATATTCACTTAACCTCATTCACTTTGAG 1080  
|||||  
1081 GAGTGTCTGTGAAGACTACTGAGAAACACCATCATCACTAAGTGAAGAAATGATGATACC 1140  
|||||  
1081 GAGTGTCTGTGAAGACTACTGAGAAACACCATCATCACTAAGTGAAGAAATGATGATACC 1140  
|||||  
1141 ATCTTCCAAAATCCTATGTTACAGAGCTATACGAATGGGTTCAGTTCAAGGACATT 1200  
|||||  
1141 ATCTTCCAAAATCCTATGTTACAGAGCTATACGAATGGGTTCAGTTCAAGGACATT 1200  
|||||  
1201 AAAAAAATATGAGGAAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTTGAGGTT 1260  
|||||  
1201 AAAAAAATATGAGGAAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTTGAGGTT 1260  
|||||  
1261 CTGGTTGCAAGTCTAGTGAATGCTAGAAAGACAGATATGCAAGATGAGTCAAGTCAAGTCA 1320  
|||||  
1261 CTGGTTGCAAGTCTAGTGAATGCTAGAAAGACAGATATGCAAGATGAGTCAAGTCAAGTCA 1320  
|||||  
1321 TCATTACAGAAAGAGATTAGTACTGAAGAGCAGCTAAGGCGCTGCAAGAGGAGAGCTT 1380  
|||||  
1321 TCATTACAGAAAGAGATTAGTACTGAAGAGCAGCTAAGGCGCTGCAAGAGGAGAGCTT 1380  
|||||  
1381 TGCAAAATCTGATGATAGAAATATGCTATCGTTTTTGTCTTCTGTCGACATCTAGTC 1440  
|||||  
1381 TGCAAAATCTGATGATAGAAATATGCTATCGTTTTTGTCTTCTGTCGACATCTAGTC 1440  
|||||  
1441 ACTTGTAAACAATGCTCTGAAGCAGTTGACAAGTGCCTGCAAGTGCACAGTCACTACT 1500  
|||||  
1441 ACTTGTAAACAATGCTCTGAAGCAGTTGACAAGTGCCTGCAAGTGCACAGTCACTACT 1500  
|||||  
1501 TTCAAGCAAAAAATTTTATGCTTAACTTAATCTAATCTATAGTAGGCAATGTTATCTTCTCT 1560  
|||||  
1501 TTCAAGCAAAAAATTTTATGCTTAACTTAATCTAATCTATAGTAGGCAATGTTATCTTCTCT 1560  
|||||  
1561 TATTACCCCTGATTGAATGTTGATGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1620  
|||||  
1561 TATTACCCCTGATTGAATGTTGATGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1620  
|||||  
1621 TAGCATTGCTACCAAGTAGGAAAAAATGATACATGAGGAGTGTGTTAGTGGCAATATA 1680  
|||||  
1621 TAGCATTGCTACCAAGTAGGAAAAAATGATACATGAGGAGTGTGTTAGTGGCAATATA 1680  
|||||  
1681 ATCTTTTGAATTTCTGATTTTTCAGGGTATAGCTGATATATCCATTTTTTACTGTTA 1740  
|||||  
1681 ATCTTTTGAATTTCTGATTTTTCAGGGTATAGCTGATATATCCATTTTTTACTGTTA 1740  
|||||  
1741 TTTAAATGAAACCATAGACTAAGAAATGAAGACATCATATCACTAATCACTGAACAAATGTGT 1800  
|||||  
1741 TTTAAATGAAACCATAGACTAAGAAATGAAGACATCATATCACTAATCACTGAACAAATGTGT 1800  
|||||  
1801 ATTCATAGTATCTGATTTAAATTTCTAAGTGAAGTGAATTAATCATCTCGATTTTTTAT 1860  
|||||

Db 1801 ATTCATAGTATCTGATTTAAATTTCTAAGTGAAGTGAATTAATCATCTCGATTTTTTAT 1860  
QY 1861 TCCTTTTCAGATAGGCTTAACAAAATGAGCTTTCTGTATATAAAATGTTGAGATAGAGTTA 1920  
Db 1861 TCCTTTTCAGATAGGCTTAACAAAATGAGCTTTCTGTATATAAAATGTTGAGATAGAGTTA 1920  
QY 1921 ATCTCCCAATCAATTAATTTGTGTTGTGAAAAAGGAATAAATTTGTTCCATGCTGGTG 1980  
Db 1921 ATCTCCCAATCAATTAATTTGTGTTGTGAAAAAGGAATAAATTTGTTCCATGCTGGTG 1980  
QY 1981 GAAAGATAGAGATTGTTTTTAGAGTTGGTGTGTTTTTAGGATTCTCTCAATTTCT 2040  
Db 1981 GAAAGATAGAGATTGTTTTTAGAGTTGGTGTGTTTTTAGGATTCTCTCAATTTCT 2040  
QY 2041 TTTAAAGTTATAAACAAGTACTTTGTGCGAATTAATTTTTTAAAGTATTGTTCCATTTTG 2100  
Db 2041 TTTAAAGTTATAAACAAGTACTTTGTGCGAATTAATTTTTTAAAGTATTGTTCCATTTTG 2100  
QY 2101 AAAGCGTATTAAATGATAGAAATCTATCGAGCCAAACATGTACTGACATGGAAGATGCTA 2160  
Db 2101 AAAGCGTATTAAATGATAGAAATCTATCGAGCCAAACATGTACTGACATGGAAGATGCTA 2160  
QY 2161 AAGATATGTTAAGTGTAAATGCAAGTGGCAAAACACTATGTTAGTCTGAGCCAGATCA 2220  
Db 2161 AAGATATGTTAAGTGTAAATGCAAGTGGCAAAACACTATGTTAGTCTGAGCCAGATCA 2220  
QY 2221 AACTATGATGTTTTTAAATGATAGAAATGCAAGTGGCAAAAGATTTGAAAGATATACACAACTG 2280  
Db 2221 AAGTATGATGTTTTTAAATGATAGAAATGCAAGTGGCAAAAGATTTGAAAGATATACACAACTG 2280  
QY 2281 TTAATGTTGTTTCTCTTCGGGAGGGGGGATTGGGGAGGGGGCCAGAGGGGTTTTA 2340  
Db 2281 TTAATGTTGTTTCTCTTCGGGAGGGGGGATTGGGGAGGGGGCCAGAGGGGTTTTA 2340  
QY 2341 TAGGGGCTTTTCACTTTTCTACCTTTTCTATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2400  
Db 2341 TAGGGGCTTTTCACTTTTCTACCTTTTCTATTTTCTCTCTCTCTCTCTCTCTCTCTCTCT 2400  
QY 2401 GTATTACTTTGTTAAATCAGAAATTTTGAAGATTTTGTCTGATTTTAAAGCTTTAGGCA 2460  
Db 2401 GTATTACTTTGTTAAATCAGAAATTTTGAAGATTTTGTCTGATTTTAAAGCTTTAGGCA 2460  
QY 2461 GTTCAACGCTGCAAACTTACTTATCCTCAGCTTACTTCTAGTTTCTTCTAATCAAGAGGCA 2520  
Db 2461 GTTCAACGCTGCAAACTTACTTATCCTCAGCTTACTTCTAGTTTCTAATCAAGAGGCA 2520  
QY 2521 GGGCAGTTAACCTTTTGTGCGCAATGTAAGTGAATGTAAGTGAATGTAAGTGAATGTAAGT 2580  
Db 2521 GGGCAGTTAACCTTTTGTGCGCAATGTAAGTGAATGTAAGTGAATGTAAGTGAATGTAAGT 2580  
QY 2581 TGTGGATGAAAAATATTTCTGAGTGGTATTTTGTGACAGTACAGCTGCTTATCTCTG 2640  
Db 2581 TGTGGATGAAAAATATTTCTGAGTGGTATTTTGTGACAGTACAGCTGCTTATCTCTG 2640  
QY 2641 TTTCAAAATGAATTTCTGATTTTGTAAATGAAATATAAAATATGCTCTCAGATCTTCC 2700  
Db 2641 TTTCAAAATGAATTTCTGATTTTGTAAATGAAATATAAAATATGCTCTCAGATCTTCC 2700  
QY 2701 AATTAAATAGTAGGATTCACTCTTAATCTCTGTTAGTTTAAAGCTGCTTAAAGTCACTTT 2760  
Db 2701 AATTAAATAGTAGGATTCACTCTTAATCTCTGTTAGTTTAAAGCTGCTTAAAGTCACTTT 2760  
QY 2761 ACTTAAAGATCTTTGTTAACTCAGTATTTTAAACATCTGTCAGCTTATGAGTGAAGT 2820  
Db 2761 ACTTAAAGATCTTTGTTAACTCAGTATTTTAAACATCTGTCAGCTTATGAGTGAAGT 2820  
QY 2821 AGAAGCATGTTTGTACACTGCTTGTAGTTATAGTGACAGCTTTCCATGTTGAGATTCTCA 2880  
Db 2821 AGAAGCATGTTTGTACACTGCTTGTAGTTATAGTGACAGCTTTCCATGTTGAGATTCTCA 2880  
QY 2881 TATCATCTTGTATCTTAAAGTTTCTATGTGAGTTTTTACCCTTAGGATGATTAAAGATGAT 2940  
Db 2881 TATCATCTTGTATCTTAAAGTTTCTATGTGAGTTTTTACCCTTAGGATGATTAAAGATGAT 2940



||||| GCTACTCGGAGGCTGAGGAGGAGATGTTGTAACCGGAGGAGAGCTTGCAGTGA 5160  
Db 5101  
||||| GCGAGATCTCGGACTGCACTCGAGCTGGGCAACAGACAGACTCTCTCAAAAAA 5220  
QY 5161  
||||| GCGAGATCTCGGACTGCACTCGAGCTGGGCAACAGACAGACTCTCTCAAAAAA 5220  
Db 5161  
AAAAA 5232  
QY 5221  
AAAAA 5232  
Db 5221  
RESULT 3  
HS167P19/c 122742 bp DNA linear HTG 10-JUL-2001  
LOCUS Homo sapiens chromosome X clone RP1-167P19 map q25, \*\*\* SEQUENCING  
DEFINITION IN PROGRESS \*\*\*, 10 unordered pieces.  
ACCESSION Z93014  
VERSION Z93014.2 GI:10045109  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_CANCELLED.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 122742)  
Grafham,D.  
Direct Submission  
Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
requests: clonequests@sanger.ac.uk  
On Sep 9, 2000 this sequence version replaced gi:6981883.  
----- Genome Center  
Center: Sanger Centre  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: humquery@sanger.ac.uk  
----- Project Information  
Center project name: dj167p19  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Sequencing vector: M13; M7815; 18% of reads  
Chemistry: Dye-terminator ABI; 100% of reads  
Consensus quality: 118637 bases at least Q40  
Consensus quality: 119897 bases at least Q30  
Consensus quality: 120866 bases at least Q20  
Insert size: 121842; sum-of-contigs  
Quality coverage: 6.65x in Q20 bases; sum-of-contigs  
-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 10 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved  
\* 1 18344: contig of 18344 bp in length  
\* 18345 18444: gap of 100 bp  
\* 18445 24822: contig of 6378 bp in length  
\* 24823 24922: gap of 100 bp  
\* 24923 26984: contig of 2062 bp in length  
\* 26985 27084: gap of 100 bp  
\* 27085 36741: contig of 9657 bp in length  
\* 36742 36841: gap of 100 bp  
\* 36842 40798: contig of 3957 bp in length  
\* 40799 40898: gap of 100 bp  
\* 40899 50764: contig of 9866 bp in length  
\* 50765 50864: gap of 100 bp  
\* 50865 60908: contig of 10044 bp in length  
\* 60909 61008: gap of 100 bp  
\* 61009 90700: contig of 29692 bp in length  
\* 90701 90800: gap of 100 bp

\* 90801 101526: contig of 10726 bp in length  
\* 101527 101626: gap of 100 bp  
\* 101627 122742: contig of 21116 bp in length.  
FEATURES  
source  
1..122742  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="X"  
/map="q25"  
/clone="RP1-167P19"  
/clone\_lib="RPC1-1"  
1..18344  
/note="assembly\_fragment:00897  
fragment\_chain:1"  
18445..24822  
/note="assembly\_fragment:03100  
fragment\_chain:1"  
24923..26984  
/note="assembly\_fragment:01003  
fragment\_chain:2"  
27085..36741  
/note="assembly\_fragment:01036  
fragment\_chain:2"  
36842..40798  
/note="assembly\_fragment:02480  
fragment\_chain:3"  
40899..50764  
/note="assembly\_fragment:02098  
fragment\_chain:3"  
50865..60908  
/note="assembly\_fragment:00356"  
61009..90700  
/note="assembly\_fragment:00910"  
90801..101526  
/note="assembly\_fragment:02458"  
101627..122742  
/note="assembly\_fragment:02641"  
BASE COUNT 34749 a 24137 c 25101 g 37853 t 902 others  
ORIGIN  
Query Match 67.3%; Score 3523; DB 2; Length 122742;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 3893; Conservative 0; Mismatches 5; Indels 1; Gaps 1;  
QY 1332 AGAGATTAGTACTGAAGCAGCAGTAAAGCCCTCAAGAGAGAGAGCTTTCACAAATCTG 1391  
Db 88530 AGAGATTAGTACTGAAGCAGCAGTAAAGCCCTCAAGAGAGAGAGCTTTCACAAATCTG 88471  
QY 1392 TATGGATAGAAATATTGCTATCGTTTTTGTCTTGTGGACATCTAGTCTACTTGTAAACA 1451  
Db 88470 TATGGATAGAAATATTGCTATCGTTTTTGTCTTGTGGACATCTAGTCTACTTGTAAACA 88411  
QY 1452 ATGTGCTGAAGCAGTGTGACAAGTGTCCATGTGTACACAGTCAATTAATTTCAAGCAAAA 1511  
Db 88410 ATGTGCTGAAGCAGTGTGACAAGTGTCCATGTGTACACAGTCAATTAATTTCAAGCAAAA 88351  
QY 1512 AATTTTATGCTTTAATCTAACTATATAGTAGGATGTTATGTTGTTCTTATTAATCCCTGA 1571  
Db 88350 AATTTTATGCTTTAATCTAACTATATAGTAGGATGTTATGTTGTTCTTATTAATCCCTGA 88291  
QY 1572 TTGAATGTGTGATGTGAAGTGAAGTAAATAGTAAATCAGGATTAATCCATTAAGCAATTTGCT 1631  
Db 88290 TTGAATGTGTGATGTGAAGTGAAGTAAATAGTAAATCAGGATTAATCCATTAAGCAATTTGCT 88231  
QY 1632 ACCAAGTAGGAAAAAATAATGTACATGGCAGTGTGTTTATAGTGGCAATATAATCTTTGAAT 1691  
Db 88230 ACCAAGTAGGAAAAAATAATGTACATGGCAGTGTGTTTATAGTGGCAATATAATCTTTGAAT 88171  
QY 1692 TCTTGATTTTTCAGGGTATTAGCTGTATTATCCATTTTCTTACTGTATTATTAATGAAA 1751  
Db 88170 TCTTGATTTTTCAGGGTATTAGCTGTATTATCCATTTTCTTACTGTATTATTAATGAAA 88111  
QY 1752 CCATAGACTAAGAATAAGAAGCATCATATACTATAAATACTGAACACAAATGTGTATTATAGTAT 1811

Db 88110 CCAATAGACTAAGATAAAGCAGCATCATATACTATACTGAACCAATGCTGTATTCATAGTAT 88051  
Qy 1812 ACTGATTTAAATTTCTAAGCTGAAGTGAATTAATCATCTGGATTTTAAATCTTTTCAGAT 1871  
Db 88050 ACTGATTTAAATTTCTAAGCTGAAGTGAATTAATCATCTGGATTTTAAATCTTTTCAGAT 87991  
Qy 1872 AGGCTTAACAAATGGAGCTTTCTGTATATAAAATGTGGAGATAGAGTAAATCTCCCCAAT 1931  
Db 87990 AGGCTTAACAAATGGAGCTTTCTGTATATAAAATGTGGAGATAGAGTAAATCTCCCCAAT 87931  
Qy 1932 CACATAATTTGTTGTGTGAAAAAGGAAATAAATGTTCATGCTGTGGGAAAGATAGAG 1991  
Db 87930 CACATAATTTGTTGTGTGAAAAAGGAAATAAATGTTCATGCTGTGGGAAAGATAGAG 87871  
Qy 1992 ATTGTTTATAGAGTTGGTGTGTGTTTATAGGATTCGTCCATTTCTTTTAAAGTTAT 2051  
Db 87870 ATTGTTTATAGAGTTGGTGTGTGTTTATAGGATTCGTCCATTTCTTTTAAAGTTAT 87811  
Qy 2052 AAACACGTACTGTGCGAATTAATTTTAAAGTGATTTGCCATTTTGAAGCGTATTT 2111  
Db 87810 AAACACGTACTGTGCGAATTAATTTTAAAGTGATTTGCCATTTTGAAGCGTATTT 87751  
Qy 2112 AATGATAGAACTACTGAGCCCAACATGCTACTGACATGGAAGATGTCAAAGATATGTTA 2171  
Db 87750 AATGATAGAACTACTGAGCCCAACATGCTACTGACATGGAAGATGTCAAAGATATGTTA 87691  
Qy 2172 AGTGTAAATGCAAGTGCAGCAACACTATGATAGTCTGAGCCAGATCAAAAGTATGATG 2231  
Db 87690 AGTGTAAATGCAAGTGCAGCAACACTATGATAGTCTGAGCCAGATCAAAAGTATGATG 87631  
Qy 2232 TTTTAAATGATGATAGAACAAAGATTTGGAAGATATACACCAAACTGTTAAATGTGGT 2291  
Db 87630 TTTTAAATGATGATAGAACAAAGATTTGGAAGATATACACCAAACTGTTAAATGTGGT 87571  
Qy 2292 TTCTCTCGGGAGGGGGGATTTGGGGAGGGGCCCCAGAGGGGTTTATAGGGCCCTTT 2351  
Db 87570 TTCTCTCGGGAGGGGGGATTTGGGGAGGGGCCCCAGAGGGGTTTATAGGGCCCTTT 87511  
Qy 2352 TCACCTTTCTACTTTTTCATTTTGTCTGTTTCGAAATTTTATAAGTATGTTATACATTTT 2411  
Db 87510 TCACCTTTCTACTTTTTCATTTTGTCTGTTTCGAAATTTTATAAGTATGTTATACATTTT 87451  
Qy 2412 GTAATCAGAAATTTTAGAAATATTTTCTGATTTAAAGGCTTAGGCAATGTTCAACGCC 2471  
Db 87450 GTAATCAGAAATTTTAGAAATATTTTCTGATTTAAAGGCTTAGGCAATGTTCAACGCC 87391  
Qy 2472 TGCAAACTACTTATCACTCAGCTTTAGTCTTCTAATCCAGAGGAGGAGGAGTTAAC 2531  
Db 87390 TGCAAACTACTTATCACTCAGCTTTAGTCTTCTAATCCAGAGGAGGAGGAGTTAAC 87331  
Qy 2532 CTTTGTGTGCCAATGTGAAATGTAATGATTTTATGTTTTCCTGCTTTTGTGGATGAAA 2591  
Db 87330 CTTTGTGTGCCAATGTGAAATGTAATGATTTTATGTTTTCCTGCTTTTGTGGATGAAA 87271  
Qy 2592 AATATTTCTAGTGTGATTTTTCAGAGGTAGACCATGCTTATCTGTTTTCAAAATAA 2651  
Db 87270 AATATTTCTAGTGTGATTTTTCAGAGGTAGACCATGCTTATCTGTTTTCAAAATAA 87211  
Qy 2652 GTATTTCTGATTTTCTAATAAGAAATATAAATATGCTCAGATCTTCCAATTAATAGT 2711  
Db 87210 GTATTTCTGATTTTCTAATAAGAAATATAAATATGCTCAGATCTTCCAATTAATAGT 87151  
Qy 2712 AAGGATTCATCTTAATCTTGTAGTTTAAAGCCTGCTTAAGTCACTTTACTAAAAAGATC 2771  
Db 87150 AAGGATTCATCTTAATCTTGTAGTTTAAAGCCTGCTTAAGTCACTTTACTAAAAAGATC 87091  
Qy 2772 TTTGTTAACTCAGTATTTTAAACATCTGTACAGCTTATGTAGTAAAAAGTAGAAGCATGTT 2831  
Db 87090 TTTGTTAACTCAGTATTTTAAACATCTGTACAGCTTATGTAGTAAAAAGTAGAAGCATGTT 87031  
Qy 2832 TGTACACTGCTTGTAGTTATAGTACAGCTTTTCCATGTTGAGATTCATATCATCTTGT 2891  
Db 87030 TGTACACTGCTTGTAGTTATAGTACAGCTTTTCCATGTTGAGATTCATATCATCTTGT 85891

Db 87030 TGTACACTGCTTGTAGTTATAGTACAGCTTTTCCATGTTGAGATTCCTCATATCATCTTGT 86971  
Qy 2892 ATCTTAAAGTTTTCATGTGAGTTTACCGTTAGGATGATTAAGATGTATATAGACAAAA 2951  
Db 86970 ATCTTAAAGTTTTCATGTGAGTTTACCGTTAGGATGATTAAGATGTATATAGACAAAA 86911  
Qy 2952 TGTAAAGTCTTCTCTACCTACATTTGTTTCTTGGCTAGTAATAAGTAGTAGTACTTTC 3011  
Db 86910 TGTAAAGTCTTCTCTACCTACATTTGTTTCTTGGCTAGTAATAAGTAGTAGTACTTTC 86851  
Qy 3012 TGAATTAATCTTCTCAAGATCCTTAAACCTCTTGGAAATTTATAAAATATTTGGCAA 3071  
Db 86850 TGAATTAATCTTCTCAAGATCCTTAAACCTCTTGGAAATTTATAAAATATTTGGCAA 86791  
Qy 3072 GAAAAGAAAGATAGTGTGTTTAAATATTTTAAAAACACTTGAATAAGAAATCAGTAGGG 3131  
Db 86790 GAAAAGAAAGATAGTGTGTTTAAATATTTTAAAAACACTTGAATAAGAAATCAGTAGGG 86731  
Qy 3132 TATAAAGTGAAGTTTAAAAATGCTCATAGAAAGTCCAGGGTTTACATTAACAAGATTTCT 3191  
Db 86730 TATAAAGTGAAGTTTAAAAATGCTCATAGAAAGTCCAGGGTTTACATTAACAAGATTTCT 86671  
Qy 3192 CACAACAAACCATTTGTAGAGGTGAGTAAGCATGTTTACTACAGAGGAAAGTGTGAGAGT 3251  
Db 86670 CACAACAAACCATTTGTAGAGGTGAGTAAGCATGTTTACTACAGAGGAAAGTGTGAGAGT 86611  
Qy 3252 AAAAAGTGAAGAAATATATTTTGTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3311  
Db 86610 AAAAAGTGAAGAAATATATTTTGTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 86551  
Qy 3312 TCCTAACTTCTGTGATTTACTTAAAGTGATATTCATTTAAACATTTGCAAAATTTATTT 3371  
Db 86550 TCCTAACTTCTGTGATTTACTTAAAGTGATATTCATTTAAACATTTGCAAAATTTATTT 86491  
Qy 3372 TTATTTTAAATTTTCTTTTGTAGATGAGTCTTGTGTTGTCACCCAGGCTGGAGTGAG 3431  
Db 86490 TTATTTTAAATTTTCTTTTGTAGATGAGTCTTGTGTTGTCACCCAGGCTGGAGTGAG 86431  
Qy 3432 TGGAGTGTATCTCTGCTCACTCAACCTCCGCTTCTGCTTCTGCTTCTGCTGCTC 3491  
Db 86430 TGGAGTGTATCTCTGCTCACTCAACCTCCGCTTCTGCTTCTGCTTCTGCTGCTC 86371  
Qy 3492 AGCTTCTGTAGTACGTGGAAATTTACAGGAGGTGGCACCACCTGCTGCTGCTGCTT 3551  
Db 86370 AGCTTCTGTAGTACGTGGAAATTTACAGGAGGTGGCACCACCTGCTGCTGCTGCTT 86311  
Qy 3552 TTTTGTAGTAGAGCGGGTTTTCACCATGTTGGCAGGCTGCTGATCAAACTCCTGACCTCA 3611  
Db 86310 TTTTGTAGTAGAGCGGGTTTTCACCATGTTGGCAGGCTGCTGATCAAACTCCTGACCTCA 86251  
Qy 3612 AGAGATCCACTCGCTTCCCTCCCAAGTCTGGATTTACAGGCTTGAGCCACCAACGCC 3671  
Db 86250 AGAGATCCACTCGCTTCCCTCCCAAGTCTGGATTTACAGGCTTGAGCCACCAACGCC 86191  
Qy 3672 CGGCTAAACATTTGCAAAATTTAAATGAGATTTTAAAAATTAATAATGACCTGCTGTT 3731  
Db 86190 CGGCTAAACATTTGCAAAATTTAAATGAGATTTTAAAAATTAATAATGACCTGCTGTT 86131  
Qy 3732 TCTGTTTGTAGTATGTAATCTCTGCTTCTTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 3791  
Db 86130 TCTGTTTGTAGTATGTAATCTCTGCTTCTTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 86071  
Qy 3792 TTATATAGTCAATTAACCTGAAATTTGGTCTGTATAGTCTAGACTTTAAATTTAAAGTTTTC 3851  
Db 86070 TTATATAGTCAATTAACCTGAAATTTGGTCTGTATAGTCTAGACTTTAAATTTAAAGTTTTC 86011  
Qy 3852 TACAAGGGGAGAAAGTGTAAAAATTTTAAAAATATGTTTTCAGGACACTTCACTTCCA 3911  
Db 86010 TACAAGGGGAGAAAGTGTAAAAATTTTAAAAATATGTTTTCAGGACACTTCACTTCCA 85951  
Qy 3912 ACTCAGGTAGTGTCAATCTAGTTGTTACCCAGGACTCAAGGACTGAATTTGTTTAA 3971  
Db 85950 ACTCAGGTAGTGTCAATCTAGTTGTTACCCAGGACTCAAGGACTGAATTTGTTTAA 85891

QY 3972 CATAAGCCTTTTCTGTTCTGGAGCGCACATTTCAATTAATAATTTCTTAATAACTTTGTATG 4031  
|||||  
Db 85890 CATAAGCCTTTTCTGTTCTGGAGCGCACATTTCAATTAATAATTTCTTAATAACTTTGTATG 85831  
QY 4032 TTTAGAGTTAAGCAAGACTTTTTTCTCTCCATCCATGAGTTGGAATTTAATGACAA 4091  
|||||  
Db 85830 TTTAGAGTTAAGCAAGACTTTTTTCTCTCCATCCATGAGTTGGAATTTAATGACAA 85771  
QY 4092 CGCTGATGTGGCTAACAGTTATTTTAAAGATTTGTTAGAAATGCTTTCAGGTT 4151  
|||||  
Db 85770 CGCTGATGTGGCTAACAGTTATTTTAAAGATTTGTTAGAAATGCTTTCAGGTT 85711  
QY 4152 CTTAAATCACTCAGCAGCTCCAACTTCTAATCAAAATTTTGGAGACTTAACAGCATTTGT 4211  
|||||  
Db 85710 CTTAAATCACTCAGCAGCTCCAACTTCTAATCAAAATTTTGGAGACTTAACAGCATTTGT 85651  
QY 4212 CTGCTGTTGAACATAAAGAGCCGAGCTTTTCCATCAATTAATCCGCAAAATTTGATCA 4271  
|||||  
Db 85650 CTGCTGTTGAACATAAAGAGCCGAGCTTTTCCATCAATTAATCCGCAAAATTTGATCA 85591  
QY 4272 TTTGCAAGTCAAAACATAGCCATATCCAAATCTTTTCCCTCCCAAGAGTTCTCAGT 4331  
|||||  
Db 85590 TTTGCAAGTCAAAACATAGCCATATCCAAATCTTTTCCCTCCCAAGAGTTCTCAGT 85531  
QY 4332 GTCTACATGTAGACTATTTCTCTGTATAAAGTTCACTCTAGGATTTCAAGTCACAC 4391  
|||||  
Db 85530 GTCTACATGTAGACTATTTCTCTGTATAAAGTTCACTCTAGGATTTCAAGTCACAC 85471  
QY 4392 TTAATTTACATTTTATGTCATGCAAGATTTCAAGTAGTTTTCATTAAGTACTTATCTTTA 4451  
|||||  
Db 85470 TTAATTTACATTTTATGTCATGCAAGATTTCAAGTAGTTTTCATTAAGTACTTATCTTTA 85411  
QY 4452 TTTGTAATAATTTAGTCTGTGATCAAAAGCATTTGCTTAATTTTTCAGAACCTGGTTTA 4511  
|||||  
Db 85410 TTTGTAATAATTTAGTCTGTGATCAAAAGCATTTGCTTAATTTTTCAGAACCTGGTTTA 85351  
QY 4512 GCATTTACAAACTAAATTCAGTTTAAATTAATAGCTTATATTCCTTTCTCTGCTAC 4571  
|||||  
Db 85350 GCATTTACAAACTAAATTCAGTTTAAATTAATAGCTTATATTCCTTTCTCTGCTAC 85291  
QY 4572 ATTTGGTTTTTCCCTGTCCTTTGATAGCGGCTAAGGTAGGTTAAGANNNGGTTAG 4631  
|||||  
Db 85290 ATTTGGTTTTTCCCTGTCCTTTGATAGCGGCTAAGGTAGGTTAAGANNNGGTTAG 85232  
QY 4632 TGAGTGATATAAGTCAATTTGGCCCTGTGATATATATTTTGTATTTTCTTTCTTA 4691  
|||||  
Db 85231 TGAGTGATATAAGTCAATTTGGCCCTGTGATATATATTTTGTATTTTCTTTCTTA 85172  
QY 4692 TATTATTTACATTTTCAGTAGTTGTTTTTGTGTTTCCATTTTAGGGGATAAAATTTGTAT 4751  
|||||  
Db 85171 TATTATTTACATTTTCAGTAGTTGTTTTTGTGTTTCCATTTTAGGGATAAAATTTGTAT 85112  
QY 4752 TTTGAACATGAATGGAGACTACCGCCCGCAGCATTTGTTACATGATATACCCCTTTAAA 4811  
|||||  
Db 85111 TTTGAACATGAATGGAGACTACCGCCCGCAGCATTTGTTACATGATATACCCCTTTAAA 85052  
QY 4812 CCGGAATCATTGTTTTATTTCTGATTTACACAGTGTGTAATGGGGAAGGGGCTAGTAT 4871  
|||||  
Db 85051 CCGGAATCATTGTTTTATTTCTGATTTACACAGTGTGTAATGGGGAAGGGGCTAGTAT 84992  
QY 4872 ATCAGTAGGATATATCTGGATGTATATATATCATTTGCTGTTTAGAGAAATGAAATAAA 4931  
|||||  
Db 84991 ATCAGTAGGATATATCTGGATGTATATATATCATTTGCTGTTTAGAGAAATGAAATAAA 84932  
QY 4932 TGGGGCTGGCTCAGTGGCTCAGCCCTGTAAATCCAGCAGCTTTGGGAGGCTGAGGCAGGT 4991  
|||||  
Db 84931 TGGGGCTGGCTCAGTGGCTCAGCCCTGTAAATCCAGCAGCTTTGGGAGGCTGAGGCAGGT 84872  
QY 4992 GGATCAGAGGTGAGGAGATCGAGACCATCTCTGGCTAACAGGTTGAACCCCTCTCTAC 5051  
|||||  
Db 84871 GGATCAGAGGTGAGGAGATCGAGACCATCTCTGGCTAACAGGTTGAACCCCTCTCTAC 84812

QY 5052 TAAAAACAGAAAAATTAGCCGGCGTGTGGCGGGCCCTGTAGTCCAGTACTCCGGA 5111  
|||||  
Db 84811 TAAAAACAGAAAAATTAGCCGGCGTGTGGCGGGCCCTGTAGTCCAGTACTCCGGA 84752  
QY 5112 GGCTGAGGCGAGGAATGGTGTGAACCCGGGAGGCGAGCTTGAGTGGCGGAGATCTC 5171  
|||||  
Db 84751 GGCTGAGGCGAGGAATGGTGTGAACCCGGGAGGCGAGCTTGAGTGGCGGAGATCTC 84692  
QY 5172 GCCACTGCATCTCCAGCTGGGCAACAGAGCAAGACTCTGTCTCAAAAAAATAAAAA 5230  
|||||  
Db 84691 GCCACTGCATCTCCAGCTGGGCAACAGAGCAAGACTCTGTCTCAAAAAAATAAAAA 84633

RESULT 4  
HSDJ315G1 133391 bp DNA linear PRI 23-JUN-2000  
LOCUS  
DEFINITION  
Human DNA sequence from clone Rpl-315G1 on chromosome Xq24-25.  
Contains a PDZ (DHR, GLGF) domain protein pseudogene, the API3 gene  
for apoptosis inhibitor 3 (XIAP, HILP), a putative novel gene,  
ESTs, STSs, GSSs and a putative CpG island, complete sequence.

ACCESSION  
AL121601  
VERSION  
AL121601.13 GI:7159760  
KEYWORDS  
HFG; API3; CpG island; DHR; GLGF; HILP; PDZ; XIAP.  
SOURCE  
human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 133391)  
Direct Submission  
Grafham.D.  
TITLE  
Submitted (12-APR-2000) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
JOURNAL  
requests: clonerequest@sanger.ac.uk  
COMMENT  
On Mar 6, 2000 this sequence version replaced gi:6983378.  
During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variation annotation may not be found in the sequence submission  
corresponding to the overlapping clone, as we submit sequences with  
only a small overlap as described above.  
This sequence has been finished according to sequence map criteria  
as follows. An attempt is made to resolve all sequencing problems,  
such as compressions and repeats, but not necessarily within known  
annotated human repeat sequence elements (e.g. Alu). Where the  
sequence is ambiguous, there is an annotation using the 'unsure'  
feature key.  
The following abbreviations are used to associate primary accession  
numbers given in the feature table with their source databases:  
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information  
on the WORMPEP database can be found at  
http://www.sanger.ac.uk/Projects/C-elegans/wormpep This sequence  
was generated from part of bacterial clone contigs of human  
chromosome X, constructed by the Sanger Centre Chromosome X Mapping  
Group. Further information can be found at  
http://www.sanger.ac.uk/HGP/ChrX  
Rpl-315G1 is from the library RPLC1-1 constructed at the Roswell  
Park Cancer Institute by the group of Pieter de Jong. For further  
details see http://bacpac.med.buffalo.edu/  
VECTOR: pCYPAC2  
This sequence is the entire insert of clone RPL-315G1 The true  
right end of clone RP6-30A23 is at 100 in this sequence.

FEATURES  
source  
1..133391  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="X"  
/map="q24-25"  
/clone="Rpl-315G1"  
/clone\_lib="RPLC1-1"  
complement(3738..4224)  
/note="match: GSS: Em:AQ85645"  
complement(4112..4623)  
/note="match: GSS: Em:AQ623859"

misc\_feature  
misc\_feature





QY 1332 AGAGATTAGTACTGAAGAGCAGCTAAGCGCCTGCAAGAGGAGAAGCTTTGCAAAATCTG 1391  
|||||  
Db 35108 AGAGATTAGTACTGAAGAGCAGCTAAGCGCCTGCAAGAGGAGAAGCTTTGCAAAATCTG 35167  
QY 1392 TATGGATAGAAATATTCGTATCGTGTGTTTGTTCCTTTGTGGACATCTAGTCACTTGTAAACA 1451  
|||||  
Db 35168 TATGGATAGAAATATTCGTATCGTGTGTTTGTTCCTTTGTGGACATCTAGTCACTTGTAAACA 35227  
QY 1452 ATGTGCTGAAGCAGTTGACAAGTGTCCATGTGCTACACAGTCAATTAATTTCAAGCAAAA 1511  
|||||  
Db 35228 ATGTGCTGAAGCAGTTGACAAGTGTCCATGTGCTACACAGTCAATTAATTTCAAGCAAAA 35287  
QY 1512 AATTTTATGTCTTAATCTAACTATATAGGCGATGTTATGTGTGTTCTTATTAATCCCTGA 1571  
|||||  
Db 35288 AATTTTATGTCTTAATCTAACTATATAGGCGATGTTATGTGTGTTCTTATTAATCCCTGA 35347  
QY 1572 TTGAATGTGTGATGTAACGTGACCTTTAAGTAATCAGGATTAATCCATAGCAATTTGCT 1631  
|||||  
Db 35348 TTGAATGTGTGATGTAACGTGACCTTTAAGTAATCAGGATTAATCCATAGCAATTTGCT 35407  
QY 1632 ACCAAGTAGGAAAAAATGTACATGCGAGTGTGTTTGTAGTTGGCAATATAATCTTTGAAT 1691  
|||||  
Db 35408 ACCAAGTAGGAAAAAATGTACATGCGAGTGTGTTTGTAGTTGGCAATATAATCTTTGAAT 35467  
QY 1692 TCTTGATTTTTCAGGGTATTAGCTGTATTATCCATTTTTTTTACTGTTATTAATTTGAAA 1751  
|||||  
Db 35468 TCTTGATTTTTCAGGGTATTAGCTGTATTATCCATTTTTTTTACTGTTATTAATTTGAAA 35527  
QY 1752 CCATAGACTAAGAAATAGAGCAGCATCACTATAACTGAACACAATGTATTCATAGTAT 1811  
|||||  
Db 35528 CCATAGACTAAGAAATAGAGCAGCATCACTATAACTGAACACAATGTATTCATAGTAT 35587  
QY 1812 ACTGATTTAATTTCTAAGTGTAACTGAATTAATCATCTGGATTTTTTATCTTTTCAGAT 1871  
|||||  
Db 35588 ACTGATTTAATTTCTAAGTGTAACTGAATTAATCATCTGGATTTTTTATCTTTTCAGAT 35647  
QY 1872 AGGCTTAACAAATGGAGCTTTCTGTATATAAATGTGGAGATTAGAGTTAATCTCCCAAT 1931  
|||||  
Db 35648 AGGCTTAACAAATGGAGCTTTCTGTATATAAATGTGGAGATTAGAGTTAATCTCCCAAT 35707  
QY 1932 CACATAATTTGTTTGTGNAAGGAATAAATTTGTCATGCTGGTGGNAAGATAGAG 1991  
|||||  
Db 35708 CACATAATTTGTTTGTGNAAGGAATAAATTTGTCATGCTGGTGGNAAGATAGAG 35767  
QY 1992 ATTTGTTTTAGAGTTGGTGTCTGTGTTTAGGATTCCTGCTCAATTTCTTTTAAAGTTAT 2051  
|||||  
Db 35768 ATTTGTTTTAGAGTTGGTGTCTGTGTTTAGGATTCCTGCTCAATTTCTTTTAAAGTTAT 35827  
QY 2052 AAACACGTACTGTGCGAATTAATTTTTTAAAGTGATTTGCCATTTTGAAGCGTATTT 2111  
|||||  
Db 35828 AAACACGTACTGTGCGAATTAATTTTTTAAAGTGATTTGCCATTTTGAAGCGTATTT 35887  
QY 2112 AATGATAGATATCTATCGAGCCACATGTACTGACATGGAAGATGCAAGATATGTTA 2171  
|||||  
Db 35888 AATGATAGATATCTATCGAGCCACATGTACTGACATGGAAGATGCAAGATATGTTA 35947  
QY 2172 AGTGAAAAATGCAAGTGGCAAAACACATATGATAGTGTGAGCCAGATCAAAAGTATGTATG 2231  
|||||  
Db 35948 AGTGAAAAATGCAAGTGGCAAAACACATATGATAGTGTGAGCCAGATCAAAAGTATGTATG 36007  
QY 2232 TTTTAAATATGCAATAGAACAAAAGATTGGAAAGATATACACCAAACTGTTTAAATGTGGT 2291  
|||||  
Db 36008 TTTTAAATATGCAATAGAACAAAAGATTGGAAAGATATACACCAAACTGTTTAAATGTGGT 36067  
QY 2292 TTCTCTCGGGAGGGGGGATTTGGGGAGGGGGCCCCAGAGGGGTTTTATAGGGGCTTT 2351  
|||||  
Db 36068 TTCTCTCGGGAGGGGGGATTTGGGGAGGGGGCCCCAGAGGGGTTTTATAGGGGCTTT 36127  
QY 2352 TCACCTTCTACTTTTTCATTTTCTCTGTTTCGAATTTTTTATAGATATGTAATTTT 2411  
|||||  
Db 36128 TCACCTTCTACTTTTTCATTTTCTCTGTTTCGAATTTTTTATAGATATGTAATTTT 36187

QY 2412 GTAATCAGAAATTTTATAGAAAGTATTTTGTCTGATTTTAAAGGCTTAGGCAATGTTCAAAAGCC 2471  
|||||  
Db 36188 GTAATCAGAAATTTTATAGAAAGTATTTTGTCTGATTTTAAAGGCTTAGGCAATGTTCAAAAGCC 36247  
QY 2472 TGCAAAACACTACTTATCACTCAGCTTTAGTTTTCTAATCCAAAGAGCGCAGGCGAGTTAAC 2531  
|||||  
Db 36248 TGCAAAACACTACTTATCACTCAGCTTTAGTTTTCTAATCCAAAGAGCGCAGGCGAGTTAAC 36307  
QY 2532 CTTTTCCTGGTGCCTAATGTGAAATGTAAATGATTTTATGTTTCTGCTGCTTTGCGATGAAA 2591  
|||||  
Db 36308 CTTTTCCTGGTGCCTAATGTGAAATGTAAATGATTTTATGTTTCTGCTGCTTTGCGATGAAA 36367  
QY 2592 AATATTTCTGAGTGGTATGTTTTTTTGACAGGTAGACCATGTCTTATCTTTGTTTCAAAAATAA 2651  
|||||  
Db 36368 AATATTTCTGAGTGGTATGTTTTTTTGACAGGTAGACCATGTCTTATCTTTGTTTCAAAAATAA 36427  
QY 2652 GTATTTCTGATTTTGTAAATGAAATATATAAATATGCTCAGATCTTCCCAATTAATTAGT 2711  
|||||  
Db 36428 GTATTTCTGATTTTGTAAATGAAATATATAAATATGCTCAGATCTTCCCAATTAATTAGT 36487  
QY 2712 AAGGATTCATCTCTTAATCTTGTAGTTTAAAGCCTGCTAAGTCACTTTACTTAAAGATC 2771  
|||||  
Db 36488 AAGGATTCATCTCTTAATCTTGTAGTTTAAAGCCTGCTAAGTCACTTTACTTAAAGATC 36547  
QY 2772 TTTGTTAACTCAGTATTTTAAACATCTGTCAAGTCTTATGTAGTAAAAAGTAGAAGCATGPT 2831  
|||||  
Db 36548 TTTGTTAACTCAGTATTTTAAACATCTGTCAAGTCTTATGTAGTAAAAAGTAGAAGCATGPT 36607  
QY 2832 TGTACACTGCTTTGATTTATAGTGCACAGCTTTTCCATGTTGAGATTCATCATCTTGT 2891  
|||||  
Db 36608 TGTACACTGCTTTGATTTATAGTGCACAGCTTTTCCATGTTGAGATTCATCATCTTGT 36667  
QY 2892 ATCTTAAAGTTTCATGTGAGTTTTTACCGTTAGGATGATTAAGATGATATAGGACAAAA 2951  
|||||  
Db 36668 ATCTTAAAGTTTCATGTGAGTTTTTACCGTTAGGATGATTAAGATGATATAGGACAAAA 36727  
QY 2952 TGTGTAAGTCTTCTCTACCTACATTTGTTTTCTTGGCTAGTAATAGTAGTAGATCTTC 3011  
|||||  
Db 36728 TGTGTAAGTCTTCTCTACCTACATTTGTTTTCTTGGCTAGTAATAGTAGTAGATCTTC 36787  
QY 3012 TGAATAAATGTTCTCTCAAGATCCTTTAAACCCCTTTGGAAATTTATAAATAATTTGGCAA 3071  
|||||  
Db 36788 TGAATAAATGTTCTCTCAAGATCCTTTAAACCCCTTTGGAAATTTATAAATAATTTGGCAA 36847  
QY 3072 GAAAAGGAAGATAGTGTGTTTAAATATTTTAAAAACACCTTGAATAAGATCAAGTAGG 3131  
|||||  
Db 36848 GAAAAGGAAGATAGTGTGTTTAAATATTTTAAAAACACCTTGAATAAGATCAAGTAGG 36907  
QY 3132 TATAAAGTAGAAGTTTAAAAATGCTCATAGAACGTCACAGGTTTACATTAAGAGTTCT 3191  
|||||  
Db 36908 TATAAAGTAGAAGTTTAAAAATGCTCATAGAACGTCACAGGTTTACATTAAGAGTTCT 36967  
QY 3192 CACAACAAACCCATGTAGAGGTGAGTAAGCATGTTACTACAGAGGAAGTTTGGAGAT 3251  
|||||  
Db 36968 CACAACAAACCCATGTAGAGGTGAGTAAGCATGTTACTACAGAGGAAGTTTGGAGAT 37027  
QY 3252 AAAAAGTAAAAAATATATTTTGTGTTTCTAAGAGAAAGATGTTGTTATGTTTC 3311  
|||||  
Db 37028 AAAAAGTAAAAAATATATTTTGTGTTTCTAAGAGAAAGATGTTGTTATGTTTC 37087  
QY 3312 TCCTAAGTCTGTTGATTTACTTAAAGTATATTCATTTTAAACATTTGCAAAATTTAT 3371  
|||||  
Db 37088 TCCTAAGTCTGTTGATTTACTTAAAGTATATTCATTTTAAACATTTGCAAAATTTAT 37147  
QY 3372 TTATTTATTTAAATTTCTTTTGTAGATGAGTCTGTTGTCACCCAGGCTGGAGTGCAG 3431  
|||||  
Db 37148 TTATTTATTTAAATTTCTTTTGTAGATGAGTCTGTTGTCACCCAGGCTGGAGTGCAG 37207  
QY 3432 TGGAGTGATCTCTGCTCACTGCAACCTCCGCTTCTGTTGTTCAAGCGATTTCTCGTGCCTC 3491  
|||||  
Db 37208 TGGAGTGATCTCTGCTCACTGCAACCTCCGCTTCTGTTGTTCAAGCGATTTCTCGTGCCTC 37267  
QY 3492 AGCTTCCTGAGTAGCTGGAATTTACAGGCGAGGTGCCACCATGCCCGACTAAATTTTTTTTA 3551





Chemistry: Dye-terminator Big Dye; 0% of reads  
 Chemistry: Dye-terminator ABI; 96% of reads  
 Chemistry: Dye-primer-amersham; 2% of reads  
 Chemistry: Dye-primer Big Dye; 0% of reads  
 Consensus quality: 194333 bases at least Q40  
 Consensus quality: 196512 bases at least Q30  
 Consensus quality: 198047 bases at least Q20  
 Insert size: 199797; sum-of-ctontigs  
 Quality coverage: 6.87x in Q20 bases; sum-of-ctontigs  
 -----

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 15 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

\* I 4154: contig of 4154 bp in length  
 \* 4155 4254: gap of 100 bp  
 \* 4255 18703: contig of 14449 bp in length  
 \* 18704 18803: gap of 100 bp  
 \* 18804 20941: contig of 2138 bp in length  
 \* 20942 21041: gap of 100 bp  
 \* 21042 34907: contig of 13866 bp in length  
 \* 34908 35012: gap of 105 bp  
 \* 35013 37508: contig of 2496 bp in length  
 \* 37509 37608: gap of 100 bp  
 \* 37609 52739: contig of 15131 bp in length  
 \* 52740 52839: gap of 100 bp  
 \* 52840 56933: contig of 4094 bp in length  
 \* 56934 57033: gap of 100 bp  
 \* 57034 88245: contig of 31212 bp in length  
 \* 88246 88346: gap of 101 bp  
 \* 88347 93386: contig of 5040 bp in length  
 \* 93387 93486: gap of 100 bp  
 \* 93487 123956: contig of 30470 bp in length  
 \* 123957 124056: gap of 100 bp  
 \* 124057 147917: contig of 23861 bp in length  
 \* 147918 148017: gap of 100 bp  
 \* 148018 176236: contig of 28219 bp in length  
 \* 176237 176336: gap of 100 bp  
 \* 176337 187128: contig of 10792 bp in length  
 \* 187129 187228: gap of 100 bp  
 \* 187229 190824: contig of 3596 bp in length  
 \* 190825 190959: gap of 135 bp  
 \* 190960 201197: contig of 10238 bp in length.

## FEATURES

source

Location/Qualifiers

1. .201197  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="X"  
 /clone="RP3-424J12"  
 /clone\_lib="RPC1-3"  
 1. .4154  
 /note="assembly\_fragment:02486  
 fragment\_chain:1"  
 4255. 18703  
 /note="assembly\_fragment:04764  
 fragment\_chain:1"  
 18804. .20941  
 /note="assembly\_fragment:03282  
 fragment\_chain:2"  
 21042. .34907  
 /note="assembly\_fragment:03624  
 fragment\_chain:2"  
 35008. .37508  
 /note="assembly\_fragment:00340"  
 37609. .52739  
 /note="assembly\_fragment:00671.0"  
 52840. .56933  
 /note="assembly\_fragment:01287.0"  
 57034. .88245

misc\_feature

misc\_feature

misc\_feature

misc\_feature

misc\_feature

misc\_feature

misc\_feature

/note="assembly\_fragment:01294"  
 88346. .93386  
 /note="assembly\_fragment:01608"  
 93487. .123956  
 /note="assembly\_fragment:03234"  
 124057. .147917  
 /note="assembly\_fragment:04074"  
 148018. .176236  
 /note="assembly\_fragment:04816"  
 176337. 187128  
 /note="assembly\_fragment:05488"  
 187229. .190824  
 /note="assembly\_fragment:05572.0"  
 190925. .201197  
 /note="assembly\_fragment:03867  
 clone\_end:T7  
 vector\_side:right"  
 BASE COUNT 55207 a 43266 c 43712 g 57504 t 1508 others  
 ORIGIN

Query Match 67.3%; Score 3523; DB 2; Length 201197;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 3893; Conservative 0; Mismatches 5; Indels 1; Gaps 1;  
 QY 1332 AGAGATTAGTACTGAAGAGCAGCTAAGCGCCTCGAAGAGAGAGCTTTCCAAAATCTG 1391  
 Db 154178 AGAGATTAGTACTGAAGAGCAGCTAAGCGCCTCGAAGAGAGAGCTTTCCAAAATCTG 154119  
 QY 1392 TATGGATAGAAATATTCGTATCGTTTGTTCCTTGTGGACATCTAGTCACCTTGTAAACA 1451  
 Db 154118 TATGGATAGAAATATTCGTATCGTTTGTTCCTTGTGGACATCTAGTCACCTTGTAAACA 154059  
 QY 1452 ATGTGCTGAAGCAGCTTGACAAAGTGTCCCATGCTGTACACAGCTCATTTCAAGCAAAA 1511  
 Db 154058 ATGTGCTGAAGCAGCTTGACAAAGTGTCCCATGCTGTACACAGCTCATTTCAAGCAAAA 153999  
 QY 1512 AATTTTATGTCCTTAATCTAATCTATAGTAGGCGATGTTATGTTGCTCTTATTAACCTGTA 1571  
 Db 153998 AATTTTATGTCCTTAATCTAATCTATAGTAGGCGATGTTATGTTGCTCTTATTAACCTGTA 153939  
 QY 1572 TTGAATGTGTGATGTGAACCTGACCTTTAAGTAATCAGGATTAATTCCTTCAATAGCATTTGCT 1631  
 Db 153938 TTGAATGTGTGATGTGAACCTGACCTTTAAGTAATCAGGATTAATTCCTTCAATAGCATTTGCT 153879  
 QY 1632 ACCAAGTAGGAAAAAATGTACATGGCAGTGTTTGTAGTGGCAATATAATCTTTGAATT 1691  
 Db 153878 ACCAAGTAGGAAAAAATGTACATGGCAGTGTTTGTAGTGGCAATATAATCTTTGAATT 153819  
 QY 1692 TCTTGATTTTTCAGGGTATTAGCTGTATATCCATTTTTTTTACTGTTTATTAATTAATGAAA 1751  
 Db 153818 TCTTGATTTTTCAGGGTATTAGCTGTATATCCATTTTTTTTACTGTTTATTAATTAATGAAA 153759  
 QY 1752 CCATAGACTAAGATAAGAACATCATATATACTGAACACAACTGTGTATTCATAGTAT 1811  
 Db 153758 CCATAGACTAAGATAAGAACATCATATATACTGAACACAACTGTGTATTCATAGTAT 153699  
 QY 1812 ACTGATTTAATTTCTAAGTGAAGTGAATTAATCATCTGGATTTTTTTTCTTTTTCAGAT 1871  
 Db 153698 ACTGATTTAATTTCTAAGTGAAGTGAATTAATCATCTGGATTTTTTTTCTTTTTCAGAT 153639  
 QY 1872 AGGCTTAACAAATGGAGCTTTCTGTATATAAATGTGGAGATTAGAGTTAAATCTCCCCAAT 1931  
 Db 153638 AGGCTTAACAAATGGAGCTTTCTGTATATAAATGTGGAGATTAGAGTTAAATCTCCCCAAT 153579  
 QY 1932 CACATAAATTTGTTGTGTGAAAAAGGAATAAATGTTTCCATGCTGCTGGGGAAGATAGAG 1991  
 Db 153578 CACATAAATTTGTTGTGTGAAAAAGGAATAAATGTTTCCATGCTGCTGGGGAAGATAGAG 153519  
 QY 1992 ATTGTTTTTAGAGTTGGTTCTTGTGTTTATAGGATCTGTCCATTTCTTTTAAAGTTAT 2051  
 Db 153518 ATTGTTTTTAGAGTTGGTTCTTGTGTTTATAGGATCTGTCCATTTCTTTTAAAGTTAT 153459  
 QY 2052 AACACAGTACTGTGCGGAATTTATTTTAAAGTATTGTCATTTTGTGAAAGCGTATTT 2111

|||||  
Db 153458 AAACGCTACTGTGCGAATTTATTTTAAAGTGATTTGCCATTTTGAAGCGTATTT 153399  
QY 2112 AATGATAGAACTACTGACGCAACATCTGACATGGAAGATGTCGAAGATATGTTA 2171  
Db 153398 AATGATAGAACTACTGACGCAACATCTGACATGGAAGATGTCGAAGATATGTTA 153339  
QY 2172 AGTGTAAATGCAAGTGGCAAACTACTATGATAGTCTGAGCCAGATCAAAAGTATGTATG 2231  
Db 153338 AGTGTAAATGCAAGTGGCAAACTACTATGATAGTCTGAGCCAGATCAAAAGTATGTATG 153279  
QY 2232 TTTTAAATGATAGAACAAAGATTTGGAAAGATATACACCAAACTGTTAAATGTGGT 2291  
Db 153278 TTTTAAATGATAGAACAAAGATTTGGAAAGATATACACCAAACTGTTAAATGTGGT 153219  
QY 2292 TTTCTCTCGGGAGGGGGGATTTGGGAGGGGGCCCGAGAGGGGTTTATAGGGCCCTTT 2351  
Db 153218 TTTCTCTCGGGAGGGGGGATTTGGGAGGGGGCCCGAGAGGGGTTTATAGGGCCCTTT 153159  
QY 2352 TCACCTTCTACTTTTTTCAATTTGTTCTGTTCTCGAATTTTTTATAGTATGATTAATCTTTT 2411  
Db 153158 TCACCTTCTACTTTTTTCAATTTGTTCTGTTCTCGAATTTTTTATAGTATGATTAATCTTTT 153099  
QY 2412 GTAATCAGAAATTTTGAAGATTTTTCGTGATTTTAAAGGCTTAGGCATGTTCAAACGCC 2471  
Db 153098 GTAATCAGAAATTTTGAAGATTTTTCGTGATTTTAAAGGCTTAGGCATGTTCAAACGCC 153039  
QY 2472 TGCAAACTACTTATCACTCAGCTTTAGTCTTCTTAATCCAGAGGCGAGGCGAGTTAAC 2531  
Db 153038 TGCAAACTACTTATCACTCAGCTTTAGTCTTCTTAATCCAGAGGCGAGGCGAGTTAAC 152979  
QY 2532 CTTTTTGGTGCAATGTGAAATGTAAATGATTTATGTTTTTCTGCTTTTGTGAATGAAA 2591  
Db 152978 CTTTTTGGTGCAATGTGAAATGTAAATGATTTATGTTTTTCTGCTTTTGTGAATGAAA 152919  
QY 2592 AATATTTCTGAGTGTAGTTTTTGGACAGGTAGACCATGTCTTATCTGTTTCAAATTAATAGT 2651  
Db 152918 AATATTTCTGAGTGTAGTTTTTGGACAGGTAGACCATGTCTTATCTGTTTCAAATTAATAGT 152859  
QY 2652 GTATTTCTGATTTTCTAAAGTAAATATAAATATGTCAGATCTTCCATTAATTAATAGT 2711  
Db 152858 GTATTTCTGATTTTCTAAAGTAAATATAAATATGTCAGATCTTCCATTAATTAATAGT 152799  
QY 2712 AAGGATTCATCCTTAATCCTTGCTAGTTTAAAGCCTGCGCTAAAGTCACTTTACTTAAAGATC 2771  
Db 152798 AAGGATTCATCCTTAATCCTTGCTAGTTTAAAGCCTGCGCTAAAGTCACTTTACTTAAAGATC 152739  
QY 2772 TTTGTTAACTCAGTATTTTAAACATCTGTACAGCTTATGTAGGTAAAGTAAAGCATGTT 2831  
Db 152738 TTTGTTAACTCAGTATTTTAAACATCTGTACAGCTTATGTAGGTAAAGTAAAGCATGTT 152679  
QY 2832 TGTACACTGCTTGTAGTTATAGTGACAGCTTTCCATGTTTGAGATCTCATATCATCTTGT 2891  
Db 152678 TGTACACTGCTTGTAGTTATAGTGACAGCTTTCCATGTTTGAGATCTCATATCATCTTGT 152619  
QY 2892 ATCTTAAAGTTTCATGTGAGTTTTTACCCTTAGGATGATTAAGATGTATATAGGACAAA 2951  
Db 152618 ATCTTAAAGTTTCATGTGAGTTTTTACCCTTAGGATGATTAAGATGTATATAGGACAAA 152559  
QY 2952 TGTAAAGTCTTTCCTCTACCTACATTTGTTTTCTTGGCTAGTAAATAGTAGTACATCTC 3011  
Db 152558 TGTAAAGTCTTTCCTCTACCTACATTTGTTTTCTTGGCTAGTAAATAGTAGTACATCTC 152499  
QY 3012 TGAATAAATGTTCTCTCAAGATCTTAAACCTCTTGGAAATTAATAAATATTTGGCAA 3071  
Db 152498 TGAATAAATGTTCTCTCAAGATCTTAAACCTCTTGGAAATTAATAAATATTTGGCAA 152439  
QY 3072 GAAAAGAGAATAGTGTGTTTAAATATTTTTTAAAAACACCTTGAATAAGAATCAGTAGGG 3131  
Db 152438 GAAAAGAGAATAGTGTGTTTAAATATTTTTTAAAAACACCTTGAATAAGAATCAGTAGGG 152379  
QY 3132 TATAAATAGAGTTTTAAATGCTTCATAGAACCTCCAGGGTTTACATTAACAAGATTTCT 3191  
|||||

Db 152378 TATAAATAGAGTTTTAAATGCTTCATAGAACCTCCAGGGTTTACATTAACAAGATTTCT 152319  
QY 3192 CACAACAACCATTTGTAGAGTGTAGTAAGCATGTCTACTACAGAGGAAAGTTTTCAGAGT 3251  
Db 152318 CACAACAACCATTTGTAGAGTGTAGTAAGCATGTCTACTACAGAGGAAAGTTTTCAGAGT 152259  
QY 3252 AAAAAGTGTAAATAATATATTTTGTGTTTCTTAAGAGAAAGAGTATTTGTTATGTTTC 3311  
Db 152258 AAAAAGTGTAAATAATATATTTTGTGTTTCTTAAGAGAAAGAGTATTTGTTATGTTTC 152199  
QY 3312 TCCTAACTCTGTTGATTTACTTAAAGTGTATATCAATTTAAACATTTGCAAAATTTAT 3371  
Db 152198 TCCTAACTCTGTTGATTTACTTAAAGTGTATATCAATTTAAACATTTGCAAAATTTAT 152139  
QY 3372 TTATTTATTTAAATTTCTTTTTGAGATGGAGTCTTGTGTCCACCAAGCTGAGGTGAG 3431  
Db 152138 TTATTTATTTAAATTTCTTTTTGAGATGGAGTCTTGTGTCCACCAAGCTGAGGTGAG 152079  
QY 3432 TGGAGTGTATCTGTCTCACTGCAACCTCCGCTTCTGGGTTTCAAGCGATTTCTGTCGCTC 3491  
Db 152078 TGGAGTGTATCTGTCTCACTGCAACCTCCGCTTCTGGGTTTCAAGCGATTTCTGTCGCTC 152019  
QY 3492 AGCTTCTGTAGTGTGGAATTTACAGGAGGTGCCACCATGCCCCGACTAAATTTTTTTTA 3551  
Db 152018 AGCTTCTGTAGTGTGGAATTTACAGGAGGTGCCACCATGCCCCGACTAAATTTTTTTTA 151959  
QY 3552 TTTTGTAGTAGAGCGGGTTTTACCATGTTGGCAGGCTGGTATCAAACTCTCGACCTCA 3611  
Db 151958 TTTTGTAGTAGAGCGGGTTTTACCATGTTGGCAGGCTGGTATCAAACTCTCGACCTCA 151899  
QY 3612 AGAGATCCACTCGCTTCCCTTCCCAAGTGTGGGATTTACAGGCTTGAGCCACACCGCC 3671  
Db 151898 AGAGATCCACTCGCTTCCCTTCCCAAGTGTGGGATTTACAGGCTTGAGCCACACCGCC 151839  
QY 3672 CGGCTAAACATTTGCAATTTAAATGAGAGTTTAAAAATTAATTAATGACTGCCCTGTT 3731  
Db 151838 CGGCTAAACATTTGCAATTTAAATGAGAGTTTAAAAATTAATTAATGACTGCCCTGTT 151779  
QY 3732 TCTGTTTTAGTATGTAAATCTCAGTTCTTCCACCTTGGCAGTGTGCACATTTAGTTGG 3791  
Db 151778 TCTGTTTTAGTATGTAAATCTCAGTTCTTCCACCTTGGCAGTGTGCACATTTAGTTGG 151719  
QY 3792 TTATATGCTAATTAATCTTGAATTTGGTCTGTATAGTCTAGACTTTAAATTTAAAGTTTC 3851  
Db 151718 TTATATGCTAATTAATCTTGAATTTGGTCTGTATAGTCTAGACTTTAAATTTAAAGTTTC 151659  
QY 3852 TACAGGGGAGAAAGTGTAAAAATTTTAAATATGTTTTCCAGGACACTTCACTTCCA 3911  
Db 151658 TACAGGGGAGAAAGTGTAAAAATTTTAAATATGTTTTCCAGGACACTTCACTTCCA 151599  
QY 3912 AGTCAGGTAGGTAGTTCAATCTAGTTGTAGCCAAAGGACTCAAGGACTGAATTTGTTTAA 3971  
Db 151598 AGTCAGGTAGGTAGTTCAATCTAGTTGTAGCCAAAGGACTCAAGGACTGAATTTGTTTAA 151539  
QY 3972 CATAAGGCTTTTCTGTTCTGGGAGCGGCACTTCAATTTAAATTTCTTAAACCTTGTATG 4031  
Db 151538 CATAAGGCTTTTCTGTTCTGGGAGCGGCACTTCAATTTAAATTTCTTAAACCTTGTATG 151479  
QY 4032 TTTAGAGTTTAAAGCAAGACTTTTTTCTTCTCCATGAGTTGTGAAATTTAATGCACAA 4091  
Db 151478 TTTAGAGTTTAAAGCAAGACTTTTTTCTTCTCCATGAGTTGTGAAATTTAATGCACAA 151419  
QY 4092 CGCTGATCTGGCTAAACAGTTTATTTTAAAGATTTGTTAGAAATGCTGTGCTTCAGGTT 4151  
Db 151418 CGCTGATCTGGCTAAACAGTTTATTTTAAAGATTTGTTAGAAATGCTGTGCTTCAGGTT 151359  
QY 4152 CTTAAAACTCAGACTCCAACTTCTAATCAAAATTTTGGAGACTTTAAACAGATTTGT 4211  
Db 151358 CTTAAAACTCAGACTCCAACTTCTAATCAAAATTTTGGAGACTTTAAACAGATTTGT 151299  
QY 4212 CTGCTGTTTGAATATAAAAGCAGGATCTTTTCCATCTAATTTCCGCAAAATTTGATCA 4271  
Db 151298 CTGCTGTTTGAATATAAAAGCAGGATCTTTTCCATCTAATTTCCGCAAAATTTGATCA 151239

QY 4272 TTTGCAAGTCAAAAGTATAGCCATATCCAAATCTTTTCCCTCCCAAGAGTTCTCAGT 4331  
|||||  
Db 151238 TTTGCAAGTCAAAAGTATAGCCATATCCAAATCTTTTCCCTCCCAAGAGTTCTCAGT 151179  
  
QY 4332 GTCTACATGTAGACTATTCCTTTTCTGTATAAAGTTCACCTCTAGGATTTCAAGTACCAC 4391  
|||||  
Db 151178 GTCTACATGTAGACTATTCCTTTTCTGTATAAAGTTCACCTCTAGGATTTCAAGTACCAC 151119  
|||||  
QY 4392 TTATTTTACATTTTAGTCATGCAAGATTCAGTGTAGTTTGTGCAATAGTACTTATCTTTA 4451  
|||||  
Db 151118 TTATTTTACATTTTAGTCATGCAAGATTCAGTGTAGTTTGTGCAATAGTACTTATCTTTA 151059  
|||||  
QY 4452 TTTGTAATAATTTAGTCTGCTGATCAAAAGCATTTGCTTTAATTTTGTAGAACTGGTTTA 4511  
|||||  
Db 151058 TTTGTAATAATTTAGTCTGCTGATCAAAAGCATTTGCTTTAATTTTGTAGAACTGGTTTA 150999  
|||||  
QY 4512 GCATTTACAACATAAATTCAGTTCAATTAATTAATAGCTTTATATGCTTTCCTGCTAC 4571  
|||||  
Db 150998 GCATTTACAACATAAATTCAGTTCAATTAATTAATAGCTTTATATGCTTTCCTGCTAC 150939  
|||||  
QY 4572 ATTTGGTTTTTCCCTGTCCTCTTGATTAACGGCTAAGGTAGGTAAGANNGGTGTAG 4631  
|||||  
Db 150938 ATTTGGTTTTTCCCTGTCCTCTTGATTAACGGCTAAGGTAGGTAAGANNGGTGTAG 150880  
|||||  
QY 4632 TGAGTGTATATAATGTGATTTGGCCCTGTGTATATATGATATTTTGTATTTTGTGTTA 4691  
|||||  
Db 150879 TGAGTGTATATAATGTGATTTGGCCCTGTGTATATATGATATTTTGTATTTTGTGTTA 150820  
|||||  
QY 4692 TATATTTACATTTACGATGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTAT 4751  
|||||  
Db 150819 TATATTTACATTTACGATGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTAT 150760  
|||||  
QY 4752 TTTGAACTATGAATGGAGACTACGCCCGACGATTTAGTTTACATGATATACCTTTAAA 4811  
|||||  
Db 150759 TTTGAACTATGAATGGAGACTACGCCCGACGATTTAGTTTACATGATATACCTTTAAA 150700  
|||||  
QY 4812 CCCGAATCATTTGTTTATTTTCTTGATTACACAGGTGTTGAATGGGAAAGGGCTAGTAT 4871  
|||||  
Db 150699 CCCGAATCATTTGTTTATTTTCTTGATTACACAGGTGTTGAATGGGAAAGGGCTAGTAT 150640  
|||||  
QY 4872 ATCAGTAGGATATACATGAGGATATATATATATCATTTGCTGTAGAGAAATGAAATAAA 4931  
|||||  
Db 150639 ATCAGTAGGATATACATGAGGATATATATATATCATTTGCTGTAGAGAAATGAAATAAA 150580  
|||||  
QY 4932 TGGGGCTGGCTCAGTGGCTCAGCCCTGTAATCCAGCACTTTGGGAGGCTGAGGCAGGT 4991  
|||||  
Db 150579 TGGGGCTGGCTCAGTGGCTCAGCCCTGTAATCCAGCACTTTGGGAGGCTGAGGCAGGT 150520  
|||||  
QY 4992 GGATCAGGAGTCAAGAGATCGAGACCATCTGCTGCTAACACGGTGAACCCCGCTCTCTAC 5051  
|||||  
Db 150519 GGATCAGGAGTCAAGAGATCGAGACCATCTGCTGCTAACACGGTGAACCCCGCTCTCTAC 150460  
|||||  
QY 5052 TAAAAACAGAAATATAGCCGGGGTGGTGGGGGGCCCTGTAGTCCAGCTACTCGGGA 5111  
|||||  
Db 150459 TAAAAACAGAAATATAGCCGGGGTGGTGGGGGGCCCTGTAGTCCAGCTACTCGGGA 150400  
|||||  
QY 5112 GGCTGAGGAGGAGATGTGTGAACCCGGGAGGAGGCTTCAGTGAGCCGAGATCTC 5171  
|||||  
Db 150399 GGCTGAGGAGGAGATGTGTGAACCCGGGAGGAGGCTTCAGTGAGCCGAGATCTC 150340  
|||||  
QY 5172 GCCACTGCACCTCCAGCCTGGGCAACAGAGCAAGACTCTGTCTCAAAAAAAGAAAAA 5230  
|||||  
Db 150339 GCCACTGCACCTCCAGCCTGGGCAACAGAGCAAGACTCTGTCTCAAAAAAAGAAAAA 150281  
|||||

RESULT 6  
AX412131  
LOCUS AX412131  
DEFINITION Sequence 231 from Patent WO0226968.  
ACCESSION AX412131  
VERSION AX412131.1 GI:21444588  
KEYWORDS

SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Korneluk, R.G., Lacasse, E., Baird, S., Holcik, M. and Young, S.  
TITLE Antisense iap nucleic acids and uses thereof  
JOURNAL Patent: WO 0226968-A 231 04-APR-2002;  
University of Ottawa (CA); Aegera Therapeutics Inc. (CA)  
FEATURES  
source Location/Qualifiers  
1..3000  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
BASE COUNT 974 a 452 c 601 g 973 t  
ORIGIN  
  
Query Match 43.5%; Score 2278; DB 6; Length 3000;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2328; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GAAAAGGTGCACAGTCTCTATTTTCAAGAGAAGATGACTTTTAACAGTCTTTGAAGGATCT 60  
|||||  
Db 657 GAAAAGGTGCACAGTCTCTATTTTCAAGAGAAGATGACTTTTAACAGTCTTTGAAGGATCT 716  
|||||  
QY 61 AAAACTTGTCTACCTGCAGACATCAATAGGAAGAAGAAATTTGTAAGAGTCTTAATAGAG 120  
|||||  
Db 717 AAAACTTGTCTACCTGCAGACATCAATAGGAAGAAGAAATTTGTAAGAGTCTTAATAGAG 776  
|||||  
QY 121 TTAATAACTTTTGTCTATTTTCCAAAGTGGTAGTCTCTTTTCAGCATCAACACTGGCAGCA 180  
|||||  
Db 777 TTAATAACTTTTGTCTATTTTCCAAAGTGGTAGTCTCTTTTCAGCATCAACACTGGCAGCA 836  
|||||  
QY 181 GCAGGTTTCTTATCTGCTGAAGGAGATACCGTGGGTGCTTTAGTTGTGTCATGCACT 240  
|||||  
Db 837 GCAGGTTTCTTATCTGCTGAAGGAGATACCGTGGGTGCTTTAGTTGTGTCATGCACT 896  
|||||  
QY 241 GTAGATAGTGGCAATATGGAGACTCAGCAGTTTGAAGACACAGAGAAAGTATCCCAAAAT 300  
|||||  
Db 897 GTAGATAGTGGCAATATGGAGACTCAGCAGTTTGAAGACACAGAGAAAGTATCCCAAAAT 956  
|||||  
QY 301 TGCAGATTTATCAACGGCTTTTATCTTTGAAAATAGTCCAGCAGTCTACAAATTTCTGGT 360  
|||||  
Db 957 TGCAGATTTATCAACGGCTTTTATCTTTGAAAATAGTCCAGCAGTCTACAAATTTCTGGT 1016  
|||||  
QY 361 ATCCAGAAATCGTCAGTCAAAAGTTGAAAACATCTCTGGGAAGCAGAGATCATTTTGCCTTA 420  
|||||  
Db 1017 ATCCAGAAATCGTCAGTCAAAAGTTGAAAACATCTCTGGGAAGCAGAGATCATTTTGCCTTA 1076  
|||||  
QY 421 GACAGGCCATCTCAGACACATGCAGACTATCTTTTGAAGACTGGCAGGTTGTAGATATA 480  
|||||  
Db 1077 GACAGGCCATCTCAGACACATGCAGACTATCTTTTGAAGACTGGCAGGTTGTAGATATA 1136  
|||||  
QY 481 TCAGACACATATACCCGAGGAACCCCTGCCATGTATAGTGAAGAGCTAGATTAAGTCC 540  
|||||  
Db 1137 TCAGACACATATACCCGAGGAACCCCTGCCATGTATTTGTGAAGAGCTAGATTAAGTCC 1196  
|||||  
QY 541 TTTTCAGAACTGGCCAGACTATGCTCAGCTAACCCCAAGAGAGTTAGCAAGTGTGGACTC 600  
|||||  
Db 1197 TTTTCAGAACTGGCCAGACTATGCTCAGCTAACCCCAAGAGAGTTAGCAAGTGTGGACTC 1256  
|||||  
QY 601 TACTACACAGTATTTGTGTACCAAGTGCAGTGTCTTTTGTGTGTGGTGAAGAACTGAAAAAT 660  
|||||  
Db 1257 TACTACACAGTATTTGTGTACCAAGTGCAGTGTCTTTTGTGTGTGGTGAAGAACTGAAAAAT 1316  
|||||  
QY 661 TGGGAACCTTGTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
|||||  
Db 1317 TGGGAACCTTGTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1376  
|||||  
QY 721 GTTTTGGCCGGGAATCTTAATATTCGAAGTGAATCTGATGCTGTGAGTCTCTGATAGGAAT 780  
|||||  
Db 1377 GTTTTGGCCGGGAATCTTAATATTCGAAGTGAATCTGATGCTGTGAGTCTCTGATAGGAAT 1436  
|||||  
QY 781 TTCCCAAAATCAACAAATCTTCCAAAGAAATCCATCCATGGCAGATTTATGAAGCAGGATC 840  
|||||

Db	1437	 TTCCCAAATTCACAAATCTTCCAGAAATCCATCCATGGCAGATTATGAAGACGAGTC	1496
Qy	841	 TTTACTTTTGGGACATGGGATATACTCAGTTTAAACAGGACGAGCTTGCAAGAGCTGGGATTT	900
Db	1497	 TTTACTTTTGGGACATGGGATATACTCAGTTTAAACAGGACGAGCTTGCAAGAGCTGGGATTT	1556
Qy	901	 TATGCTTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTTCACTCTGGAGGAGGCTAACTGAT	960
Db	1557	 TATGCTTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTTCACTCTGGAGGAGGCTAACTGAT	1616
Qy	961	 TGGAGCCCAAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCAAATAT	1020
Db	1617	 TGGAGCCCAAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCAAATAT	1676
Qy	1021	 CTGTTTAGAACAGAGGACAGAATATATAAACAAATATTCAATTAACCTCATTTCACTTTGAG	1080
Db	1677	 CTGTTTAGAACAGAGGACAGAATATATAAACAAATATTCAATTAACCTCATTTCACTTTGAG	1736
Qy	1081	 GAGTGTCTGTTAAGAATCTACTGAGAAAACACCATCACCTAACTAGAAGAAATTTGATGATACC	1140
Db	1737	 GAGTGTCTGTTAAGAATCTACTGAGAAAACACCATCACCTAACTAGAAGAAATTTGATGATACC	1796
Qy	1141	 ATCTTCCAAAATCCTATGTTACAGAAGCTATACGAATGGGGTTCAGTTTCAAGGACATTT	1200
Db	1797	 ATCTTCCAAAATCCTATGTTACAGAAGCTATACGAATGGGGTTCAGTTTCAAGGACATTT	1856
Qy	1201	 AAGAAAATATGAGGAGAAAATTCAGATATCTGGGAGCAACTATAAATCACTTTGAGGTT	1260
Db	1857	 AAGAAAATATGAGGAGAAAATTCAGATATCTGGGAGCAACTATAAATCACTTTGAGGTT	1916
Qy	1261	 CTGGTTGCAGATCTAGTGAATGCTCAGAAAGACAGTATGCAAGATGAGTCAAGTCAGACT	1320
Db	1917	 CTGGTTGCAGATCTAGTGAATGCTCAGAAAGACAGTATGCAAGATGAGTCAAGTCAGACT	1976
Qy	1321	 TCATTTACAGAAAGAGATTAGTACTGAAGACAGCTTAAGGCGCTGCAAGAGGAGGAAGCTT	1380
Db	1977	 TCATTTACAGAAAGAGATTAGTACTGAAGACAGCTTAAGGCGCTGCAAGAGGAGGAAGCTT	2036
Qy	1381	 TGCAAAATCTGTATGATAGAATATGCTATCGTTTGTGTTTCTCTGFGGACATCTAGTC	1440
Db	2037	 TGCAAAATCTGTATGATAGAATATGCTATCGTTTGTGTTTCTCTGFGGACATCTAGTC	2096
Qy	1441	 ACTGTAAACAATGTGCTGAAGCAGTTGACAAAGTCTCCATGTGCTACACAGTCAATTACT	1500
Db	2097	 ACTGTAAACAATGTGCTGAAGCAGTTGACAAAGTCTCCATGTGCTACACAGTCAATTACT	2156
Qy	1501	 TTCAAGCAAAAAATTTTATGTCTTAATCTAATCTATAGTAGGCATGTTATGTTGTTCT	1560
Db	2157	 TTCAAGCAAAAAATTTTATGTCTTAATCTAATCTATAGTAGGCATGTTATGTTGTTCT	2216
Qy	1561	 TATTACCTCGATTGAATGTGTGATGTGACTGCATTTAAGTAATCAAGATTGAATTCAT	1620
Db	2217	 TATTACCTCGATTGAATGTGTGATGTGACTGCATTTAAGTAATCAAGATTGAATTCAT	2276
Qy	1621	 TAGCATTTGCTACCAAGTAGGAAAAAATGACATGGCAGTGGTTTGTAGTTGGCAATATA	1680
Db	2277	 TAGCATTTGCTACCAAGTAGGAAAAAATGACATGGCAGTGGTTTGTAGTTGGCAATATA	2336
Qy	1681	 ATCTTTGAATTTCTGATTTTTCAGGGTATTAGCTGTATTATCCATTTTTTTTACTGTTA	1740
Db	2337	 ATCTTTGAATTTCTGATTTTTCAGGGTATTAGCTGTATTATCCATTTTTTTTACTGTTA	2396
Qy	1741	 TTTAAATGAAACCATAGACTAGAAATGAAGACATCATCTATTAACGCAACAATGTGT	1800
Db	2397	 TTTAAATGAAACCATAGACTAGAAATGAAGACATCATCTATTAACGCAACAATGTGT	2456
Qy	1801	 ATTCAVAGTATCTGATTTTAAATTTCTTAAGTGTPAAGTGAATTAATCATCTCGATTTTTAT	1860
Db	2457	 ATTCAVAGTATCTGATTTTAAATTTCTTAAGTGTPAAGTGAATTAATCATCTCGATTTTTAT	2516
Qy	1861	 TCCTTTTCAGATAGGCTTAAACAAATGGAGCTTTCTGTATATAAATGTGGAGATTAGATTA	1920

Db	2517	TCTTTTCAGATAGGGTTAAACAAATGGAGCTTTCGTATATAAATGTGGAGATTAGAGTTA	2576
Qy	1921	ATCTCCCAATCACATAATTTGTTTGTGTGAAAGGAATAAATGTTCATGCTGGTG	1980
Db	2577	ATCTCCCAATCACATAATTTGTTTGTGTGAAAGGAATAAATGTTCATGCTGGTG	2636
Qy	1981	GAAGATAGAGATTGTTTTAGAGTTGGTTGTTGTGTTTTAGGATTCGTCCATTTTCT	2040
Db	2637	GAAGATAGAGATTGTTTTAGAGTTGGTTGTTGTGTTTTAGGATTCGTCCATTTTCT	2696
Qy	2041	TTTAAAGTATTAACACAGCTACTCTGCGCAATATTTTTTAAAGTGATTTGCCATTTTGG	2100
Db	2697	TTTAAAGTATTAACACAGCTACTCTGCGCAATATTTTTTAAAGTGATTTGCCATTTTGG	2756
Qy	2101	AAAGCGTATTTAATGATAGATACTATCGAGCGCAACATGTACTGACATGGAAAGATGTCA	2160
Db	2757	AAAGCGTATTTAATGATAGATACTATCGAGCGCAACATGTACTGACATGGAAAGATGTCA	2816
Qy	2161	AAGATATGTTAAGTGTAATAATGCAAGTGGCAAAACACTATGTATAGTCTGAGCCAGATCA	2220
Db	2817	AAGATATGTTAAGTGTAATAATGCAAGTGGCAAAACACTATGTATAGTCTGAGCCAGATCA	2876
Qy	2221	AAGTATGTATGTTTTATATATGCATAGAACAAAGATTTGGAAGATATACACCAAACTG	2280
Db	2877	AAGTATGTATGTTTTATATATGCATAGAACAAAGATTTGGAAGATATACACCAAACTG	2936
Qy	2281	TTAAATGTTGTTCTCTTCGCGGAGGGGGGATTTGGGGAGGGGCCCA	2329
Db	2937	TTAAATGTTGTTCTCTTCGCGGAGGGGGGATTTGGGGAGGGGCCCA	2985
RESULT 7			
LOCUS	AX429575	2404 bp	DNA linear PAT 21-JUN-2002
DEFINITION	Sequence 38 from Patent WO0226820.		
ACCESSION	AX429575		
VERSION	AX429575.1	GI:21540833	
KEYWORDS	human.		
SOURCE	ORGANISM Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
TITLE	Cohen,D., Dengler,U.J., Finelli,A.L., Freuler,F., Konsoliaki,M.,		
JOURNAL	Reinhardt,M.W. and Zusman,S.		
FEATURES	Transgenic drosophila melanogaster expressing beta amyloid		
source	Patent: WO 0226820-A 38 04-APR-2002;		
	NOVARTIS ERFIND VERWALT GMBH (AT)		
	Location/Qualifiers		
	1..2404		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
BASE COUNT	759 a 372 c 525 g 748 t		
ORIGIN			
Query Match	38.7%;	Score 2027;	DB 6; Length 2404;
Best Local Similarity	99.9%;	Pred. No. 0;	
Matches 2317;	Conservative 0;	Mismatches 1;	Indels 2; Gaps 2;
Qy	1	GAAGAAGTGGACAAGTCCTATTTTCAAGAAGATGACTTTTAAACAGTTTGAAGGATCT	60
Db	1	GAAGAAGTGGACAAGTCCTATTTTCAAGAAGATGACTTTTAAACAGTTTGAAGGATCT	60
Qy	61	AAAACCTGTGTACCTGCAGACATCAATTAAGAAGNAGAAATTTGTAGAGAGCTTTAATAGA	120
Db	61	AAAACCTGTGTACCTGCAGACATCAATTAAGAAGNAGAAATTTGTAGAGAGCTTTAATAGA	120
Qy	121	TTAAAACTTTTGTAAATTTTCCAGTGGTAGTCTCTGTTCCAGATCAACACTGGCAGCA	180
Db	121	TTAAAACTTTTGTAAATTTTCCAGTGGTAGTCTCTGTTCCAGATCAACACTGGCAGCA	180
Qy	181	GCAGGTTTCTTTATACGTGGTGAAGGAGATACCGTGCAGGCTCTTTAGTGTGTCAGCT	240

Db	181	GCAGGGTTCTTTATACTGGTGAAGAGANACCGTGCCTTTAGTTGTCTACGAGCT	240
Qy	241	GTAGATAGATGCGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAGATATCCCAAAAT	300
Db	241	GTAGATAGATGCGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAGATATCCCAAAAT	300
Qy	301	TGCAGATTATCAACGGCTTTTATCTTGAAANATAGTCCACGCAGTCTACAAATTCFGGT	360
Db	301	TGCAGATTATCAACGGCTTTTATCTTGAAANATAGTCCACGCAGTCTACAAATTCFGGT	360
Qy	361	ATCCAGAAATCGTCAGTACAAAGTTGAAACTATCTCGGAACGACAGATCATTTTGCTTTA	420
Db	361	ATCCAGAAATCGTCAGTACAAAGTTGAAACTATCTCGGAACGACAGATCATTTTGCTTTA	420
Qy	421	GACAGGCCATCTCAGACACATCAGACTATCTTTTGAAACTGGCGAGGTGTAGATATA	480
Db	421	GACAGGCCATCTCAGACACATCAGACTATCTTTTGAAACTGGCGAGGTGTAGATATA	480
Qy	481	TCAGACACCATATACCCGAGGAACCTGCCATGTATAGTGAAGAGCTAGATTAAAGTCC	540
Db	481	TCAGACACCATATACCCGAGGAACCTGCCATGTATAGTGAAGAGCTAGATTAAAGTCC	540
Qy	541	TTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGATTAGCAAGTGTGGACTC	600
Db	541	TTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGATTAGCAAGTGTGGACTC	600
Qy	601	TACTACACAGGTATGGTGACCAAGTGCAGTCTTTTGTGTGTGGAAGAACTGAAAAAT	660
Db	601	TACTACACAGGTATGGTGACCAAGTGCAGTCTTTTGTGTGTGGAAGAACTGAAAAAT	660
Qy	661	TGGAACTTTGTATCGTGCCTGGTCAG - AACACAGGCGACACTTTCCTAATTCCTTCTT	719
Db	661	TGGAACTTTGTATCGTGCCTGGTCAGTAACTACACAGGCGACACTTTCCTAATTCCTTCTT	720
Qy	720	TGTTTTGGCGCGAATCTTAAATATTCGAAGTGAATCTGATGCTGTGAGTCTGTAGGAA	779
Db	721	TGTTTTGGCGCGAATCTTAAATATTCGAAGTGAATCTGATGCTGTGAGTCTGTAGGAA	780
Qy	780	TTTCCCAAATTCACAAATCTTCCAAAGAAATCCATCCATGGCAGATTATGAAGCACGGAT	839
Db	781	TTTCCCAAATTCACAAATCTTCCAAAGAAATCCATCCATGGCAGATTATGAAGCACGGAT	840
Qy	840	CTTTTACTTTTGGACATGGATATCTCAGTTTAAACAGGAGCAGCTTGCAGAGCTGGATT	899
Db	841	CTTTTACTTTTGGACATGGATATCTCAGTTTAAACAGGAGCAGCTTGCAGAGCTGGATT	900
Qy	900	TTATGCTTTTAGGTGAGGTCATAAAGTAAAGTGCCTTTTCACTGTGGAGGAGGCTTAAC	959
Db	901	TTATGCTTTTAGGTGAGGTCATAAAGTAAAGTGCCTTTTCACTGTGGAGGAGGCTTAAC	960
Qy	960	TTGGAAGCCAGTGAAGACCTTTGGGAACACACTGCTAAATGGTATCCAGGGTCAAAATA	1019
Db	961	TTGGAAGCCAGTGAAGACCTTTGGGAACACACTGCTAAATGGTATCCAGGGTCAAAATA	1020
Qy	1020	TCTGTTAGAACAAGGGACAAGAATATATAACAATATTCATTAACTCATTCACCTTGA	1079
Db	1021	TCTGTTAGAACAAGGGACAAGAATATATAACAATATTCATTAACTCATTCACCTTGA	1080
Qy	1080	GGAGTGTCTGGTGAAGAATCTAGAGAAAACACCATCTAATAGAGAAATGTATGATAC	1139
Db	1081	GGAGTGTCTGGTGAAGAATCTAGAGAAAACACCATCTAATAGAGAAATGTATGATAC	1140
Qy	1140	CATCTCCAAAATCCATGGTACAGAAGCTATACGAATGGGTTCAGTTTCAAGGACAT	1199
Db	1141	CATCTCCAAAATCCATGGTACAGAAGCTATACGAATGGGTTCAGTTTCAAGGACAT	1200
Qy	1200	TAAGAAAATTAATGGAGGAAAAATTCAGATATCTCGGAGCAACTATAAATCACTTCAGGT	1259
Db	1201	TAAGAAAATTAATGGAGGAAAAATTCAGATATCTCGGAGCAACTATAAATCACTTCAGGT	1260
Qy	1260	TCTGGTTGCAGATCTAGTGAATGCTCAGAAAAGACAGTATGCAAGATGAGTCAAGTCAGAC	1319
Db	1261	TCTGGTTGCAGATCTAGTGAATGCTCAGAAAAGACAGTATGCAAGATGAGTCAAGTCAGAC	1320

[illegible]



DEFINITION Sequence 1 from patent US 6087173.  
ACCESSION ARI03281  
VERSION ARI03281.1 GI:12814869  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 2540)  
AUTHORS Bennett,C.Frank., Ackermann,E.J. and Cowsert,L.M.  
TITLE Antisense modulation of x-linked inhibitor of apoptosis expression  
JOURNAL Patent: US 6087173-A 1 11-JUL-2000;  
FEATURES Location/Qualifiers  
source 1..2540  
BASE COUNT 781 a 415 c 571 g 773 t  
ORIGIN

Query Match 38.0%; Score 1990; DB 6; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAAGGTGGACAAGTCTATTTCAGAGAGAGATGACTTTTAACAGTTTGAAGGATCT 60  
DB 1 GAAAGGTGGACAAGTCTATTTCAGAGAGAGATGACTTTTAACAGTTTGAAGGATCT 60  
QY 61 AAAAATTGTGTACCTGCAGACATCAATAAGGAAGAAGAAATTTGTAGAGAGTTTAATAGA 120  
DB 61 AAAAATTGTGTACCTGCAGACATCAATAAGGAAGAAGAAATTTGTAGAGAGTTTAATAGA 120  
QY 121 TTAATAACTTTTGTCTAATTTTCCAAAGTGGTAGTCTGTTTCAGCATCAACACTGGCAGGA 180  
DB 121 TTAATAACTTTTGTCTAATTTTCCAAAGTGGTAGTCTGTTTCAGCATCAACACTGGCAGGA 180  
QY 181 GCAGGGTTCTTTTATCTGTTGAGGAGATACCGTGGGTGCTTTTGTAGTTCATGCAGCT 240  
DB 181 GCAGGGTTCTTTTATCTGTTGAGGAGATACCGTGGGTGCTTTTGTAGTTCATGCAGCT 240  
QY 241 GTAGATAGATGGCAATATGGAGACTCAGCAGTTTGAAGACACAGGAAAGTATCCCCAAAT 300  
DB 241 GTAGATAGATGGCAATATGGAGACTCAGCAGTTTGAAGACACAGGAAAGTATCCCCAAAT 300  
QY 301 TGCAGATTATCAACGGCTTTTATCTTGAATAATAGTGGCAGGAGTCTACAAATTCGGT 360  
DB 301 TGCAGATTATCAACGGCTTTTATCTTGAATAATAGTGGCAGGAGTCTACAAATTCGGT 360  
QY 361 ATCCAGAAATGTCAGTACAAAAGTTGAAAACATCTCTGGAAGCAGAGATCATTTTGCCTTA 420  
DB 361 ATCCAGAAATGTCAGTACAAAAGTTGAAAACATCTCTGGAAGCAGAGATCATTTTGCCTTA 420  
QY 421 GACAGGCCATCTGACACACATGCAGACTATCTTTTGAGAACTGGGCAGGTTGTAGATATA 480  
DB 421 GACAGGCCATCTGACACACATGCAGACTATCTTTTGAGAACTGGGCAGGTTGTAGATATA 480  
QY 481 TCAGACACCATATACCGAGGAACCTGCCATGTATAGTGAAGAAGCTAGATTAAAGTCC 540  
DB 481 TCAGACACCATATACCGAGGAACCTGCCATGTATAGTGAAGAAGCTAGATTAAAGTCC 540  
QY 541 TTTCAGAACTGGCCAGACTATGCTCACTAACCCCAAGAGAGTTAGCAAGTCTGGACTC 600  
DB 541 TTTCAGAACTGGCCAGACTATGCTCACTAACCCCAAGAGAGTTAGCAAGTCTGGACTC 600  
QY 601 TACTACACAGGATTTGGTGACCAAGTGCAGTCTTTTGTGTTGGTGGAAAACCTGAAAAAT 660  
DB 601 TACTACACAGGATTTGGTGACCAAGTGCAGTCTTTTGTGTTGGTGGAAAACCTGAAAAAT 660  
QY 661 TGGAACTTGTGATCGCTGCTGCAGACACACAGGCGACACTTTTCTTAATGCTTCTTT 720  
DB 661 TGGAACTTGTGATCGCTGCTGCAGACACACAGGCGACACTTTTCTTAATGCTTCTTT 720  
QY 721 GTTTTGGCCCGGAATCTTAATATTTCGAAGTGAATCTGATGCTGTGAGTCTCTGATAGGAAT 780  
DB 721 GTTTTGGCCCGGAATCTTAATATTTCGAAGTGAATCTGATGCTGTGAGTCTCTGATAGGAAT 780

QY 781 TTCCCAAAATTCACAAATCTTCCAAAGAAATCCATCCATGGCAGATTTATGAAGCAGGATC 840  
DB 781 TTCCCAAAATTCACAAATCTTCCAAAGAAATCCATCCATGGCAGATTTATGAAGCAGGATC 840  
QY 841 TTTACTTTTGGGACATGGATATCTCAGTTTAAAGAGAGAGCTTGAAGAGCTGGATTT 900  
DB 841 TTTACTTTTGGGACATGGATATCTCAGTTTAAAGAGAGAGCTTGAAGAGCTGGATTT 900  
QY 901 TATCTCTTAGTGGAAGTGTATAAAGTAAAGTCTTTCACCTGGAGGAGGCTTAACGTAT 960  
DB 901 TATCTCTTAGTGGAAGTGTATAAAGTAAAGTCTTTCACCTGGAGGAGGCTTAACGTAT 960  
QY 961 TGAAGCCCACTGAAGACCTTTGGGAACAACATGCTAAATGGTATCCAGGCTGCAATAT 1020  
DB 961 TGAAGCCCACTGAAGACCTTTGGGAACAACATGCTAAATGGTATCCAGGCTGCAATAT 1020  
QY 1021 CTGTAGAACAGAGGACAGAAATATATAAACAATATTCATTTAACTCATCTACTTGAG 1080  
DB 1021 CTGTAGAACAGAGGACAGAAATATATAAACAATATTCATTTAACTCATCTACTTGAG 1080  
QY 1081 GAGTGTCTGTGTAAGAACTTACTGAGAAAACACCATCACTTAAGAAATTTGATGATACC 1140  
DB 1081 GAGTGTCTGTGTAAGAACTTACTGAGAAAACACCATCACTTAAGAAATTTGATGATACC 1140  
QY 1141 ATCTTCCAAATCTCTATGTTACAAAGAGCTATACGAATGGGGTTCAGTTTCAAGGACAT 1200  
DB 1141 ATCTTCCAAATCTCTATGTTACAAAGAGCTATACGAATGGGGTTCAGTTTCAAGGACAT 1200  
QY 1201 AAGAAATATGGAGGAAAAATTCAGATATCTGGGAGCACTATAATCATCTACTTGAGTT 1260  
DB 1201 AAGAAATATGGAGGAAAAATTCAGATATCTGGGAGCACTATAATCATCTACTTGAGTT 1260  
QY 1261 CTGTTGTCAGATCTAGTGAATGCTCAGAAAACAGATATGCAAGATGAGTCAAGTCAGACT 1320  
DB 1261 CTGTTGTCAGATCTAGTGAATGCTCAGAAAACAGATATGCAAGATGAGTCAAGTCAGACT 1320  
QY 1321 TCATTACAGAAAGAGATTAGTACTGAAAGAGAGCTAAGGCGCTGCAAGAGAGGAAAGCT 1380  
DB 1321 TCATTACAGAAAGAGATTAGTACTGAAAGAGAGCTAAGGCGCTGCAAGAGAGGAAAGCT 1380  
QY 1381 TGCAAAATCTGTATGGATAGAAATATTCCTATCGTTTGTCTCTTGTGGACATCTAGTC 1440  
DB 1381 TGCAAAATCTGTATGGATAGAAATATTCCTATCGTTTGTCTCTTGTGGACATCTAGTC 1440  
QY 1441 ACTTGTAAACAATGCTGCTGAAGCAGTTGACAAGTGTCCCATGCTCACACAGTCACTACT 1500  
DB 1441 ACTTGTAAACAATGCTGCTGAAGCAGTTGACAAGTGTCCCATGCTCACACAGTCACTACT 1500  
QY 1501 TTCAAGCAAAAATTTTATGCTTTAATCTAACTCTATAGTAGGCACTGTTATGTTGTTCT 1560  
DB 1501 TTCAAGCAAAAATTTTATGCTTTAATCTAACTCTATAGTAGGCACTGTTATGTTGTTCT 1560  
QY 1561 TATTACCTGATTAATGCTGTGATGTGACTGACTTTAAGTAAATCAGGATTTGAATTCAT 1620  
DB 1561 TATTACCTGATTAATGCTGTGATGTGACTGACTTTAAGTAAATCAGGATTTGAATTCAT 1620  
QY 1621 TAGCATTTGCTPACCAAGTAGGAAAAAATGCTACATGGCAGTGTGTTAGTTGGCAATATA 1680  
DB 1621 TAGCATTTGCTPACCAAGTAGGAAAAAATGCTACATGGCAGTGTGTTAGTTGGCAATATA 1680  
QY 1681 ATCTTTGAATTTCTTGATTTTTCAGGGTATTTAGCTGTTATATCCATTTTTTTACTGTTA 1740  
DB 1681 ATCTTTGAATTTCTTGATTTTTCAGGGTATTTAGCTGTTATATCCATTTTTTTACTGTTA 1740  
QY 1741 TTTAATTTGAACCATAGACTAAGAAATTAAGAGCATCTACTATAACTGAACACAAATGTT 1800  
DB 1741 TTTAATTTGAACCATAGACTAAGAAATTAAGAGCATCTACTATAACTGAACACAAATGTT 1800  
QY 1801 ATTCATAGTACTGATTTAATTTTCTAAGTGAATTAATTAATCACTCTGATTTTTTAT 1860  
DB 1801 ATTCATAGTACTGATTTAATTTTCTAAGTGAATTAATTAATCACTCTGATTTTTTAT 1860  
QY 1861 TCCTTTTCAGATAGCTTAAACAAATGGAGCTTTCGTGTATATAAATGTGGAGATTTAGAGTTA 1920



|||||  
Db 1861 TCCTTTTCAGATAGGCTTAACAAATGGAGCTTCTGTATATAAAATGTGGAGATTAGAGTTA 1920  
QY 1921 ATCTCCCAATACATAAATTTGTTGTGGAAGAAAGGAATAATGTTCCATGCTGGTG 1980  
Db 1921 ATCTCCCAATACATAAATTTGTTGTGGAAGAAAGGAATAATGTTCCATGCTGGTG 1980  
QY 1981 GAAAGATAGAGATTGTTTTAGAGTTGGTTGTTGTTTTAGGATTCTCTCCATTTCT 2040  
Db 1981 GAAAGATAGAGATTGTTTTAGAGTTGGTTGTTGTTTTAGGATTCTCTCCATTTCT 2040  
QY 2041 T 2041  
Db 2041 T 2041  
  
RESULT 9  
AX412118  
LOCUS AX412118 2540 bp DNA linear PAT 14-JUN-2002  
DEFINITION Sequence 218 from Patent W00226968.  
ACCESSION AX412118  
VERSION AX412118.1 GI:21444581  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE Korneluk, R.G., Lacasse, E., Baird, S., Holcik, M. and Young, S.  
AUTHORS Antisense iap nucleic acids and uses thereof  
TITLE Patent: WO 0226968-A 218 04-APR-2002;  
JOURNAL University of Ottawa (CA) ; Aegera Therapeutics Inc. (CA)  
FEATURES  
1..2540  
Source /organism="Homo sapiens"  
/db\_xref="taxon:9606"  
BASE COUNT 781 a 415 c 570 g 773 t 1 others  
ORIGIN  
  
Query Match 38.0%; Score 1990; DB 6; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GAAAGGTGGACAAAGTCCTATTTTCAAGAGAAGATGACATTTTAAACAGTTTGAAGGATCT 60  
Db 1 GAAAGGTGGACAAAGTCCTATTTTCAAGAGAAGATGACATTTTAAACAGTTTGAAGGATCT 60  
QY 61 AAAACTTGTGTACCTGCAGACATCAATAAGGAAGAAGAAATTTGTAGAAGAGTTTAATAGA 120  
Db 61 AAAACTTGTGTACCTGCAGACATCAATAAGGAAGAAGAAATTTGTAGAAGAGTTTAATAGA 120  
QY 121 TTAATAACTTTTGTCTAATTTTCAAGTGGTAGTCCTGTTTTCAGCATCAACACATGGCACGA 180  
Db 121 TTAATAACTTTTGTCTAATTTTCAAGTGGTAGTCCTGTTTTCAGCATCAACACATGGCACGA 180  
QY 181 GCAGGTTTCTTTATCTGTGTAAGGAGATACCGTGGGTGCTTTAGTTGTCTATGAGCT 240  
Db 181 GCAGGTTTCTTTATCTGTGTAAGGAGATACCGTGGGTGCTTTAGTTGTCTATGAGCT 240  
QY 241 GTAGATAGATGGCAATATGGAGACTACAGAGTTGGGAAGACACAGGAAGATATCCCAAAAT 300  
Db 241 GTAGATAGATGGCAATATGGAGACTACAGAGTTGGGAAGACACAGGAAGATATCCCAAAAT 300  
QY 301 TGCAGATTTATCAACGGCTTTTATCTTGAATAGTGGCCAGCAGTCTACAAATTTCTGGT 360  
Db 301 TGCAGATTTATCAACGGCTTTTATCTTGAATAGTGGCCAGCAGTCTACAAATTTCTGGT 360  
QY 361 ATCCAGATGGTCAGTACAAAGTTGAAACTATCTGGGAAGCAGAGATCATTTTGGCTTA 420  
Db 361 ATCCAGATGGTCAGTACAAAGTTGAAACTATCTGGGAAGCAGAGATCATTTTGGCTTA 420  
QY 421 GACAGGCCATCTGAGACACATGCAGACTATCTTTTGGAGAACTGGGAGGTTGTAGATATA 480  
Db 421 GACAGGCCATCTGAGACACATGCAGACTATCTTTTGGAGAACTGGGAGGTTGTAGATATA 480

Db 421 GACAGGCCATCTGAGACACATGCAGACTATCTTTTGGAGAACTGGGAGGTTGTAGATATA 480  
QY 481 TCAGACACCATATACCCGAGGAAACCCCTGCCATGTATAGTGAAGAAAGCTAGATTAAAGTCC 540  
Db 481 TCAGACACCATATACCCGAGGAAACCCCTGCCATGTATAGTGAAGAAAGCTAGATTAAAGTCC 540  
QY 541 TTTTCAGAACTGGCCAGACTATGCTCACTAACCCCAAGAGAGTTAGCAAGTGTCTGGACT 600  
Db 541 TTTTCAGAACTGGCCAGACTATGCTCACTAACCCCAAGAGAGTTAGCAAGTGTCTGGACT 600  
QY 601 TACTACACAGGTTATGTTGACCAAGTGCAGTCTGCTTTTGTGTTGGTGAAGAACTGAAAAAT 660  
Db 601 TACTACACAGGTTATGTTGACCAAGTGCAGTCTGCTTTTGTGTTGGTGAAGAACTGAAAAAT 660  
QY 661 TGGGAACCTTTGTATGCTGCTGTCAGAACACAGAGGACACTTTCCTAATTTGCTTTCT 720  
Db 661 TGGGAACCTTTGTATGCTGCTGTCAGAACACAGAGGACACTTTCCTAATTTGCTTTCT 720  
QY 721 GTTTTGGCCGGAATCTTAATATTCGAAAGTGAATCTGATGCTGTGAGTCTCTGATAGGAAT 780  
Db 721 GTTTTGGCCGGAATCTTAATATTCGAAAGTGAATCTGATGCTGTGAGTCTCTGATAGGAAT 780  
QY 781 TTCCCAAAATTCACAAATCTTCCAAAGAAATCCATCCATGGCAGATTATGAAGCAGGATC 840  
Db 781 TTCCCAAAATTCACAAATCTTCCAAAGAAATCCATCCATGGCAGATTATGAAGCAGGATC 840  
QY 841 TTTTACTTTTGGGACATGATATATCTCAGTTAAACAGGAGCAGCTTCAAGAGCTGGATTT 900  
Db 841 TTTTACTTTTGGGACATGATATATCTCAGTTAAACAGGAGCAGCTTCAAGAGCTGGATTT 900  
QY 901 TATGCTTTTAGTGTGAAGTGTAAAGTAAAGTGTCTTCACTGTGGAGGAGGCTTAACATGAT 960  
Db 901 TATGCTTTTAGTGTGAAGTGTAAAGTAAAGTGTCTTCACTGTGGAGGAGGCTTAACATGAT 960  
QY 961 TGGAAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATTCAGGGTGAAGATAT 1020  
Db 961 TGGAAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATTCAGGGTGAAGATAT 1020  
QY 1021 CTGTTAGAACAGAGGAGCAAGAAATATATAAACAAATATTCATTTAACTCATTTCACTTTGAG 1080  
Db 1021 CTGTTAGAACAGAGGAGCAAGAAATATATAAACAAATATTCATTTAACTCATTTCACTTTGAG 1080  
QY 1081 GAGTGTCTGTTAAGAACTACTTGAGAAAACACCATCACTAACTAGAAGAAATTTGATGATACC 1140  
Db 1081 GAGTGTCTGTTAAGAACTACTTGAGAAAACACCATCACTAACTAGAAGAAATTTGATGATACC 1140  
QY 1141 ATCTTCCAAATCCTATGTTGACAAAGAGCTATACGAATGGGGTTCAGTTTCAAGGACAT 1200  
Db 1141 ATCTTCCAAATCCTATGTTGACAAAGAGCTATACGAATGGGGTTCAGTTTCAAGGACAT 1200  
QY 1201 AAGAAATAATGGAGGAAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTTGAGTT 1260  
Db 1201 AAGAAATAATGGAGGAAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTTGAGTT 1260  
QY 1261 CTGTTTGCAGATCTAGTGAATGCTCAGAAAGACAGATGCAAGATGAGTCAAGTCAAGT 1320  
Db 1261 CTGTTTGCAGATCTAGTGAATGCTCAGAAAGACAGATGCAAGATGAGTCAAGTCAAGT 1320  
QY 1321 TCATTCAGAAAGAGATTAGTACTGAAGAGCAGCTTAAGGCCCTGCAAGAGGAGAAAGCTT 1380  
Db 1321 TCATTCAGAAAGAGATTAGTACTGAAGAGCAGCTTAAGGCCCTGCAAGAGGAGAAAGCTT 1380  
QY 1381 TGCAAATCTGTATGGATAGAAATATGCTATCGTTTTTGTCTTCTGGACATCTAGTC 1440  
Db 1381 TGCAAATCTGTATGGATAGAAATATGCTATCGTTTTTGTCTTCTGGACATCTAGTC 1440  
QY 1441 ACTTGTAAACAATGCTGCTGAAGCAGTTTGACAAGTGTCCCATGCTACACAGTCAATTA 1500  
Db 1441 ACTTGTAAACAATGCTGCTGAAGCAGTTTGACAAGTGTCCCATGCTACACAGTCAATTA 1500  
QY 1501 TTCAGCAAAAAATTTTATGCTTAACTTAATCTTAATCTATAGTGGCATGTTATGTTGTTCT 1560  
Db 1501 TTCAGCAAAAAATTTTATGCTTAACTTAATCTTAATCTATAGTGGCATGTTATGTTGTTCT 1560

Qy 1561 TATTACCTGATTGAATGTGTGATGTGAACGACGACTTTAAGTAATCAGAGTTGAATTCAT 1620  
Db 1561 TATTACCTGATTGAATGTGTGATGTGAACGACGACTTTAAGTAATCAGAGTTGAATTCAT 1620  
Qy 1621 TAGCATTTGCTACCAAGTACGAAAAAATGTCATGCGAGTGTTCAGTGGCAATATA 1680  
Db 1621 TAGCATTTGCTACCAAGTACGAAAAAATGTCATGCGAGTGTTCAGTGGCAATATA 1680  
Qy 1681 ATCTTTGAATTTCTGATTTTTCAGGGTATTAGCTGTATTATCCATTTTCTACTGTTA 1740  
Db 1681 ATCTTTGAATTTCTGATTTTTCAGGGTATTAGCTGTATTATCCATTTTCTACTGTTA 1740  
Qy 1741 TTTAATTGAAACCATAGACTAAGAATAAGAGCATCATATACTATAACTGAACACAATGTGT 1800  
Db 1741 TTTAATTGAAACCATAGACTAAGAATAAGAGCATCATATACTATAACTGAACACAATGTGT 1800  
Qy 1801 ATTCTAGTATACATGATTTAATTTCTAAGTGAAGTGAATTAATCATCTGGATTTTAT 1860  
Db 1801 ATTCTAGTATACATGATTTAATTTCTAAGTGAAGTGAATTAATCATCTGGATTTTAT 1860  
Qy 1861 TCTTTTCAGATAGCTTAACAAATGGAGCTTCTGTATATAAATGTGAGATTAGAGTTA 1920  
Db 1861 TCTTTTCAGATAGCTTAACAAATGGAGCTTCTGTATATAAATGTGAGATTAGAGTTA 1920  
Qy 1921 ATCTCCCAATCACATAATTTGTTGTGTGAAAAAGGAATAAATGTCATGCTGGTG 1980  
Db 1921 ATCTCCCAATCACATAATTTGTTGTGTGAAAAAGGAATAAATGTCATGCTGGTG 1980  
Qy 1981 GAAAGATAGAGATTGTTTTCAGAGTGGTGTGTTGTTAGGATTCGTGCCAATTTCT 2040  
Db 1981 GAAAGATAGAGATTGTTTTCAGAGTGGTGTGTTGTTAGGATTCGTGCCAATTTCT 2040  
Qy 2041 T 2041  
Db 2041 T 2041

RESULT 10  
HSU45880 2540 bp mRNA linear PRI 16-FEB-1996  
LOCUS Human X-linked inhibitor of apoptosis protein XIAP mRNA, complete  
DEFINITION cds.  
ACCESSION U45880  
VERSION U45880.1 GI:1184319  
KEYWORDS  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 2540)  
AUTHORS Liston,P., Roy,N., Tamai,K., Lefebvre,C., Baird,S.,  
Cherton-Horvat,G., Farahani,R., McLean,M., Ikeda,J., MacKenzie,A.  
and Korneluk,R.G.  
TITLE Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP genes  
JOURNAL Nature 379 (6563), 349-353 (1996)  
MEDLINE 96149249  
PUBMED 852191  
REFERENCE 2 (bases 1 to 2540)  
AUTHORS Baird,S.D.  
TITLE Direct Submission  
JOURNAL Submitted (16-JAN-1996) Stephen D. Baird, Children's Hospital of Eastern Ontario, Genetics, 401 Smyth Rd., Ottawa, Ontario, K1H 8L1, Canada

FEATURES  
source  
1. .2540  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/map="xq24-25"  
/tissue\_type="brain"  
/clone\_lib="stratagene lambda2ap-II human fetal brain"  
/dev\_stage="fetal"

CDS 34. .1527  
/function="inhibition of apoptosis"  
/note="XIAP"  
/codon\_start=1  
/evidence=experimental  
/product="X-linked inhibitor of apoptosis protein"  
/protein\_id="AAC50373.1"  
/db\_xref="GI:1184320"  
/translation="MTFNSPEGKTCVPADINKEEFVEFNRLKTFANFPSPGSPVSA  
STLARGFLVTGEGDVTFCFSCAAAVDRWQYGSVGRHRKVPNCRFINGVYLENSA  
TOSTNSGIONQYKVENYLGSRDHEALDRSETHADYLLRTGOVVDISDIIYRNPAM  
YCEARLKSQFNWPDYAHLPRELASAGLYTGGQYQCFCCGGKLNKNEPCDRAWS  
EHRHPNCFVILGRNLINRSDVSSDRNFNSTNLPRNSMADYEARITFTGTWI  
YSYNNQLARAGFYALGEGDKVKCFHCGGLTDWKPSEDPWEQHAHWYPCVKYLLLEQK  
QSYINNIHLTHSLECLVTKTSLTRIDDTIFQNPWQVEAIFRMGFSFKDKIKI  
MEKIOISGSNYKSLVLAADLVNAOKDSODESSOTSLQKEISTEOLRLQBEKLC  
KICMDRNAIVFVPCGHLV7CKOAEAVDCKPMCYVTITFKQIFNS"  
misc\_feature 108. .309  
/note="encodes BIR1 (Baculovirus IAP Repeat)"  
misc\_feature 520. .723  
/note="encodes BIR2"  
misc\_feature 826. 1020  
/note="encodes BIR3"  
misc\_feature 1381. .1485  
/note="encodes Ring Zinc Finger"  
BASE COUNT 781 a 415 c 571 g 773 t  
ORIGIN  
Query Match 38.08; Score 1990; DB 9; Length 2540;  
Best Local Similarity 100.0%; Pred. NO. 0;  
Matches 2040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 GAAAGGTGGACAAAGTCTCTATTTTCAAGAGAAAGATGACTTTTAAACAGTTTGAAGGATCT 60  
Db 1 GAAAGGTGGACAAAGTCTCTATTTTCAAGAGAAAGATGACTTTTAAACAGTTTGAAGGATCT 60  
Qy 61 AAAACTTGTGTGCTGCAGACATCAATAAGAGAAAGAAATTTGTAGAGAGTTTAATAGA 120  
Db 61 AAAACTTGTGTGCTGCAGACATCAATAAGAGAAAGAAATTTGTAGAGAGTTTAATAGA 120  
Qy 121 TTAATAACTTTTGTCTAATTTTCCAAGTGGTAGTCTCTGTTTCCAGCATCAACACTGCGACA 180  
Db 121 TTAATAACTTTTGTCTAATTTTCCAAGTGGTAGTCTCTGTTTCCAGCATCAACACTGCGACA 180  
Qy 181 GCAGGGTTTCTTTATCTGTTGAAGGAGATACCGTGCCTGCTTTAGTGTGATCGACGT 240  
Db 181 GCAGGGTTTCTTTATCTGTTGAAGGAGATACCGTGCCTGCTTTAGTGTGATCGACGT 240  
Qy 241 GTAGATAGTGGCAATATGGAGACTTCAGACTTCGAGACACAGAGAAAGTATCCCCAAAT 300  
Db 241 GTAGATAGTGGCAATATGGAGACTTCAGACTTCGAGACACAGAGAAAGTATCCCCAAAT 300  
Qy 301 TGCAGATTATCAACGGCTTTTATCTTGAAATAGTGCACGAGTCTACAAAATCTCGT 360  
Db 301 TGCAGATTATCAACGGCTTTTATCTTGAAATAGTGCACGAGTCTACAAAATCTCGT 360  
Qy 361 ATCCAGAATGTCAGTACAAAGTTGAAACTATCTGGAAGCAGAGATCATTTTGGCCTTA 420  
Db 361 ATCCAGAATGTCAGTACAAAGTTGAAACTATCTGGAAGCAGAGATCATTTTGGCCTTA 420  
Qy 421 GACAGGCATCTGAGACACATGCAGACTATCTTTTGAAGTGGCAGGTTGTAGATATA 480  
Db 421 GACAGGCATCTGAGACACATGCAGACTATCTTTTGAAGTGGCAGGTTGTAGATATA 480  
Qy 481 TCAGACACCATATACCGAGGAGAACCTGCCATGTATAGTGAAGAGCTAGATTTAAAGTCC 540  
Db 481 TCAGACACCATATACCGAGGAGAACCTGCCATGTATAGTGAAGAGCTAGATTTAAAGTCC 540  
Qy 541 TTTTCAGAACTGGCCAGACTATGCTCACCTAACCCACAGAGAGTTAGCAAGTCTGGACTC 600  
Db 541 TTTTCAGAACTGGCCAGACTATGCTCACCTAACCCACAGAGAGTTAGCAAGTCTGGACTC 600  
Qy 601 TACTACAGAGTATTTGGTGACCAAGTGCAGTGTCTTTTGTGTGGTGGAAAACTGAAAAAT 660

D	b	601	TACTACACAGGATATTGGTGTGCCAAGTCGAGTGCTTTGTTGTGGTGA AACCTGAAAAAT	660
Q	y	661	TGGGAACCTTGTGATCGTGCCTGGTCAGAACACAGCGCACACTTTCCTAAATTCGCTCTTT	720
D	b	661	TGGGAACCTTGTGATCGTGCCTGGTCAGAACACAGCGCACACTTTCCTAAATTCGCTCTTT	720
Q	y	721	GTTTTGGCCGGAATCCTTAATATTCGAAGTGAACTCGATGCTGTGAGTTCCTGATAGGAAT	780
D	b	721	GTTTTGGCCGGAATCCTTAATATTCGAAGTGAACTCGATGCTGTGAGTTCCTGATAGGAAT	780
Q	y	781	TTCCCAAAATCAACAATCTTCCAAGAAATCCATCATGSCAGATATATGAAGCACCGATC	840
D	b	781	TTCCCAAAATCAACAATCTTCCAAGAAATCCATCATGSCAGATATATGAAGCACCGATC	840
Q	y	841	TTTACTTTTTGGGACATGGATATATACTCAGTTTAAACAAGSAGCAGCTTGCACAAGCTGGATTT	900
D	b	841	TTTACTTTTTGGGACATGGATATATACTCAGTTTAAACAAGSAGCAGCTTGCACAAGCTGGATTT	900
Q	y	901	TATGCTTTTAGTGAAGTGATAAAGTAAAGTGCTTTCAC TGTGGAGAGGGCTTAAC TGAT	960
D	b	901	TATGCTTTTAGTGAAGTGATAAAGTAAAGTGCTTTCAC TGTGGAGAGGGCTTAAC TGAT	960
Q	y	961	TGGAAGCCAGTCAAGACCCCTGGGAACACATGCTTAAATGGTATCCAGGGTGCAATAT	1020
D	b	961	TGGAAGCCAGTCAAGACCCCTGGGAACACATGCTTAAATGGTATCCAGGGTGCAATAT	1020
Q	y	1021	CTGTTAGAACAGAAAGGCAAGAATATATAAACAAATATTCATTTAACTCATTCAC TTGAG	1080
D	b	1021	CTGTTAGAACAGAAAGGCAAGAATATATAAACAAATATTCATTTAACTCATTCAC TTGAG	1080
Q	y	1081	GAGTGCTGGTAGAACACTACTTGAGAAAACCACATCACTAACTAGAAGAAATGATGATACC	1140
D	b	1081	GAGTGCTGGTAGAACACTACTTGAGAAAACCACATCACTAACTAGAAGAAATGATGATACC	1140
Q	y	1141	ATCTTCCAAAATCCTATGTTACAGAGCTATACGAATGGGTTCAGTTTCAAGGACATT	1200
D	b	1141	ATCTTCCAAAATCCTATGTTACAGAGCTATACGAATGGGTTCAGTTTCAAGGACATT	1200
Q	y	1201	AAGAAAATATGGAGGAAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTTGAGGTT	1260
D	b	1201	AAGAAAATATGGAGGAAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTTGAGGTT	1260
Q	y	1261	CTGGTTGCGAGTCTAGTGAATGCTCAGAAGACAGTATGCAAGATGAGTCAAGTCAGACT	1320
D	b	1261	CTGGTTGCGAGTCTAGTGAATGCTCAGAAGACAGTATGCAAGATGAGTCAAGTCAGACT	1320
Q	y	1321	TCATTACAGAAAGAGATTAGTACTGAAGACAGCTTAAGGCGCTGCAAGAGGAGAAGCTTT	1380
D	b	1321	TCATTACAGAAAGAGATTAGTACTGAAGACAGCTTAAGGCGCTGCAAGAGGAGAAGCTTT	1380
Q	y	1381	TGCAAAATCTGATGGATAGAAAATTTGCTATGCTTTTTTCTCTTGTCGACATCTAGTC	1440
D	b	1381	TGCAAAATCTGATGGATAGAAAATTTGCTATGCTTTTTTCTCTTGTCGACATCTAGTC	1440
Q	y	1441	ACTTGTAACAATTTGCTCAGAGCAGTTGACAAAGTGCCCACTGTCTACACAGATCACTACT	1500
D	b	1441	ACTTGTAACAATTTGCTCAGAGCAGTTGACAAAGTGCCCACTGTCTACACAGATCACTACT	1500
Q	y	1501	TTCAACCAAAAAATTTTTATGCTTAACTCTATAGTAGGCATGTTATGTGTCT	1560
D	b	1501	TTCAACCAAAAAATTTTTATGCTTAACTCTATAGTAGGCATGTTATGTGTCT	1560
Q	y	1561	TATTACCCGTATTGAATGTGTGATGTGAAGTAACTGAACTTAATCAGGATGGAATTCAT	1620
D	b	1561	TATTACCCGTATTGAATGTGTGATGTGAAGTAACTGAACTTAATCAGGATGGAATTCAT	1620
Q	y	1621	TAGCATTTGCTACCAAGTAGGAAAAAAAATGTATAGTGGCAGTGTTTAGTTGGCAATATA	1680
D	b	1621	TAGCATTTGCTACCAAGTAGGAAAAAAAATGTATAGTGGCAGTGTTTAGTTGGCAATATA	1680
Q	y	1681	ATCTTTGAATTTCTGATTTTTTCAGGGTATTAGCTGTATTTATCCATTTTTTTTACTGTTA	1740
D	b	1681	ATCTTTGAATTTCTGATTTTTTCAGGGTATTAGCTGTATTTATCCATTTTTTTTACTGTTA	1740

Db	1681	ATCTTTGAATTCCTGTGATTTTTCAGGGTATATAGCTGTATATATCCATTTTTTTTTTACTGTTA	1740			
Qy	1741	TTTAATCGAAACCATAGACTAAGAATTAAGAAGCATCATACTATACTGAACACAAATGTGT	1800			
Db	1741	TTTAATCGAAACCATAGACTAAGAATTAAGAAGCATCATACTATACTGAACACAAATGTGT	1800			
Qy	1801	ATTCTAGTACTAGATTTTAATTTCTAAGTGTGAAGTGAATTAATCATCTGGATTTTTTAT	1860			
Db	1801	ATTCTAGTACTAGATTTTAATTTCTAAGTGTGAAGTGAATTAATCATCTGGATTTTTTAT	1860			
Qy	1861	TCTTTTCAGATAGGCTTAACAAATGGAGCTTTCTGTATATAAATGTGGAGATTAGAGTTA	1920			
Db	1861	TCTTTTCAGATAGGCTTAACAAATGGAGCTTTCTGTATATAAATGTGGAGATTAGAGTTA	1920			
Qy	1921	ATCTCCCAATCACATAATTTTGTGTGTGAAAGGAATAAATTTGTTCCATGCTGGTG	1980			
Db	1921	ATCTCCCAATCACATAATTTTGTGTGTGAAAGGAATAAATTTGTTCCATGCTGGTG	1980			
Qy	1981	GAAGATAGAGATGTGTTTTTGTAGGTTGGTGTGTGTTTTAGGATTCGTGCCATTTTCT	2040			
Db	1981	GAAGATAGAGATGTGTTTTTGTAGGTTGGTGTGTGTTTTAGGATTCGTGCCATTTTCT	2040			
Qy	2041	T	2041			
Db	2041	T	2041			
RESULT	11					
LOCUS	BC032729	2086 bp	linear			
DEFINITION	Homo sapiens, baculoviral IAP repeat-containing 4, clone MGC:45369					
ACCESSION	IMAGE:5532247, mRNA, complete cds.					
VERSION	BC032729					
KEYWORDS	BC032729.1 GI:21619763					
SOURCE	MGC.					
ORGANISM	human.					
REFERENCE	Homo sapiens					
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
TITLE	1 (bases 1 to 2086)					
JOURNAL	Strausberg, R.					
REMARK	Direct Submission					
COMMENT	Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA					
	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>					
	Contact: MGC help desk					
	Email: <a href="mailto:cgabps-r@mail.nih.gov">cgabps-r@mail.nih.gov</a>					
	Tissue Procurement: ATCC					
	cDNA Library Preparation: Life Technologies, Inc.					
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)					
	DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland.					
	Web site: <a href="http://www.nisc.nih.gov/">http://www.nisc.nih.gov/</a>					
	Contact: <a href="mailto:nisc.mcenhgrl.nih.gov">nisc.mcenhgrl.nih.gov</a>					
	Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., McDowell, J., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., Maduro, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgon, C., Voigt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.					
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>						
Series: IRAC Plate: 69 Row: j Column: 18						
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4502142.						
FEATURES	Location/Qualifiers					
source	1..2086					

/organism="Homo sapiens"  
/db\_xref="LocusID:331"  
/db\_xref="taxon:9606"  
/clone="MGC:45369 IMAGE:5532247"  
/tissue\_type="Uterus, leiomyosarcoma"  
/clone\_lib="NIH\_MGC\_71"  
/lab\_host="DH10B"  
/note="Vector: pCMV-SPORT6"  
79..1572  
CDS  
/codon\_start=1  
/product="baculoviral IAP repeat-containing 4"  
/protein\_id="AAH32729.1"  
/db\_xref="GI:21619764"  
/translation="MTFNSPEGSKTCVPADINKEEFVEEFNRLKTFANPPSPVSA  
STLARAGFLYTGSDTVRCFSCHAADVDRMOYGDSSAVRHRKRVSPNCRFINGFYLENSA  
TQSTNSIGONGQVKVENYLGSRDHFALDRPSETHADYLLRTGOVVDISDTIYPRNPAM  
YSREARLKSQNPQDVAHLTPRELASNGLYVTGIDQVOCFCGGKLNKWEPCDRAWS  
EHRHPNCFVFLGRNLNIRSEDAVSSDRNFNSNLPNPNMADYEARIFTFGWI  
YSYNQLARAGTALGEDVKVCFHCGGGLTDWKPSEDWQEHQAWIPGCKYLLBQK  
QBYYINNHLSLEELVTRTEKTSLSLRIDDTIFQNPVMVGEAIRMGSFKDKIKI  
MEBKIQISGNSYKSLVILVADLVNAQKDSMQDESSOTSLOKEISTBEQLRLQBEKLC  
KICWDRNIALVFVPCGHLVTCQCAPAVDKCPWCYTVITPKQIFWS"  
BASE COUNT 689 a 341 c 450 g 606 t  
ORIGIN

Query Match 33.6%; Score 1757; DB 9; Length 2086;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1997; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

Qy	1	GAAGAAGTGGACAAGTCTCTATTTTCAAGAGAAGATGACTTTTAAACAGTTTGAAGGATCT	60
Db	46	GAAGAAGTGGACAAGTCTCTATTTTCAAGAGAAGATGACTTTTAAACAGTTTGAAGGATCT	105
Qy	61	AAACTTGTGTACCTGCAGACATCAATAAGGAAGAAGATTTGTAGAGAGTTTAATAGA	120
Db	106	AAACTTGTGTACCTGCAGACATCAATAAGGAAGAAGATTTGTAGAGAGTTTAATAGA	165
Qy	121	TTAAAACTTTTGTAAATTTTCCAAGTGGTAGTCTCTTTTCAGCATCAACACTGGCACGA	180
Db	166	TTAAAACTTTTGTAAATTTTCCAAGTGGTAGTCTCTTTTCAGCATCAACACTGGCACGA	225
Qy	181	GCAGGGTTCTTTTACTGTTGAAGGAGATACCGTGGGGCTTTAGTTGTCATGCAGCT	240
Db	226	GCAGGGTTCTTTTACTGTTGAAGGAGATACCGTGGGGCTTTAGTTGTCATGCAGCT	285
Qy	241	GTAGATAGTGGCAATATGGAGACTCAGCAGTTTGAAGACACAGAGAAAGTATCCCCAAAT	300
Db	286	GTAGATAGTGGCAATATGGAGACTCAGCAGTTTGAAGACACAGAGAAAGTATCCCCAAAT	345
Qy	301	TGCAGATTATCAACGGGTTTATCTTGAAATATAGTGCACGAGTGTACAAATTCGGT	360
Db	346	TGCAGATTATCAACGGGTTTATCTTGAAATATAGTGCACGAGTGTACAAATTCGGT	405
Qy	361	ATCCAGAAATGTCAGTACAAAGTTGAAACATCTCTGGGAAGCAGAGATCATTTTGCCTTA	420
Db	406	ATCCAGAAATGTCAGTACAAAGTTGAAACATCTCTGGGAAGCAGAGATCATTTTGCCTTA	465
Qy	421	GACAGGCCATCTGAGACACATGCAGACTATCTTTTGAGAACTGGCGAGTGTAGATATA	480
Db	466	GACAGGCCATCTGAGACACATGCAGACTATCTTTTGAGAACTGGCGAGTGTAGATATA	525
Qy	481	TCAGACACCATATACCGAGGAACCCCTGCCATGTATAGTGAAGAAGCTAGATTTAAAGTCC	540
Db	526	TCAGACACCATATACCGAGGAACCCCTGCCATGTATAGTGAAGAAGCTAGATTTAAAGTCC	585
Qy	541	TTTCAGAACTGGCCAGACTATGCTCACCTACCCCAAGAGAGTTAGCAAGTGGTGGACTC	600
Db	586	TTTCAGAACTGGCCAGACTATGCTCACCTACCCCAAGAGAGTTAGCAAGTGGTGGACTC	645
Qy	601	TACTACACAGGTATGTGTACAAAGTGCAGTGTCTTTTGTGTGGTGGAAAACTGAAAAAT	660
Db	646	TACTACACAGGTATGTGTACAAAGTGCAGTGTCTTTTGTGTGGTGGAAAACTGAAAAAT	705

Qy	661	TGGAAACCTTGTGATCGTGCCCTGCTCAGAACACAGGGGACACTTTTCCCTAAATGCTCTCTT	720
Db	706	TGGAAACCTTGTGATCGTGCCCTGCTCAGAACACAGGGGACACTTTTCCCTAAATGCTCTCTT	765
Qy	721	TTTTTGGCCCGGAATCTTAATATTTCGAAGTCAATCTGATGCTGTGCTGCTGATAGGAAT	780
Db	766	TTTTTGGCCCGGAATCTTAATATTTCGAAGTCAATCTGATGCTGTGCTGCTGATAGGAAT	825
Qy	781	TTCCCAAAATTCACAAATCTTTCCAAAGAAATCCATCCATGGCAGATATTGAAGACAGGATC	840
Db	826	TTCCCAAAATTCACAAATCTTTCCAAAGAAATCCATCCATGGCAGATATTGAAGACAGGATC	885
Qy	841	TTTACTTTTGGGACATGGATATCTCACTTAACAAAGGAGCAGCTTGCAGAGCTGGATTT	900
Db	886	TTTACTTTTGGGACATGGATATCTCACTTAACAAAGGAGCAGCTTGCAGAGCTGGATTT	945
Qy	901	TATCTTTAGTGAAGTGATAAAGTAAAGTGCCTTCACTCTGGAGGAGGCTTAACATGAT	960
Db	946	TATCTTTAGTGAAGTGATAAAGTAAAGTGCCTTCACTCTGGAGGAGGCTTAACATGAT	1005
Qy	961	TGGAAGCCCACTGAAGACCCCTTGGGAACAACATGCTAAATGCTATCCAGGCTGCAAAATAT	1020
Db	1006	TGGAAGCCCACTGAAGACCCCTTGGGAACAACATGCTAAATGCTATCCAGGCTGCAAAATAT	1065
Qy	1021	CTGTTAGAACAGAGGGACAAAGATATATAAACAAATATTCATTTAACTCACTTCTGAG	1080
Db	1066	CTGTTAGAACAGAGGGACAAAGATATATAAACAAATATTCATTTAACTCACTTCTGAG	1125
Qy	1081	GAGTGTCTGTTAAGAACTACTGAGAAACACCATCACTAACTAGAGAATTTGATGATACC	1140
Db	1126	GAGTGTCTGTTAAGAACTACTGAGAAACACCATCACTAACTAGAGAATTTGATGATACC	1185
Qy	1141	ATCTTCCAAATCTCTATGTTACAAGAGCTATACGAATGGGGTTCAGTTTCAAGGACATTT	1200
Db	1186	ATCTTCCAAATCTCTATGTTACAAGAGCTATACGAATGGGGTTCAGTTTCAAGGACATTT	1245
Qy	1201	AAGAAAATTAATGGAGGAAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTGAAGTT	1260
Db	1246	AAGAAAATTAATGGAGGAAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTGAAGTT	1305
Qy	1261	CTGTTGCAGATCTAGTGAATGCTCAGAAACACAGTATGCAAGATGAGTCAAGTCAAGCT	1320
Db	1306	CTGTTGCAGATCTAGTGAATGCTCAGAAACACAGTATGCAAGATGAGTCAAGTCAAGCT	1365
Qy	1321	TCATTACAGAAAGAGATTAGTACTGAGAGCAGCTAAGGCGCCTGCAAGAGGAGAAAGCTT	1380
Db	1366	TCATTACAGAAAGAGATTAGTACTGAGAGCAGCTAAGGCGCCTGCAAGAGGAGAAAGCTT	1425
Qy	1381	TGCAAAATCTGTATGGATAGAAATATTGCTATCGTTTTTGTCTTGTGGACATCTAGTC	1440
Db	1426	TGCAAAATCTGTATGGATAGAAATATTGCTATCGTTTTTGTCTTGTGGACATCTAGTC	1485
Qy	1441	ACTTGTAAACAAATGCTGTAAGCAGTGTGACAAAGTGTCCCATGTGCTACACAGTCAATTA	1500
Db	1486	ACTTGTAAACAAATGCTGTAAGCAGTGTGACAAAGTGTCCCATGTGCTACACAGTCAATTA	1545
Qy	1501	TTCAAGCAAAAAATTTTATGCTTAACTCTAATCTAGTAGGCACTGTTATGTTGTTCT	1560
Db	1546	TTCAAGCAAAAAATTTTATGCTTAACTCTAATCTAGTAGGCACTGTTATGTTGTTCT	1605
Qy	1561	TATTACCCCTGATGAATGTGTGATGTAAGTGAATTAAGTGAATTAAGTGAATTCAT	1620
Db	1606	TATTACCCCTGATGAATGTGTGATGTAAGTGAATTAAGTGAATTAAGTGAATTCAT	1665
Qy	1621	TAGCATTTGCTTACCAAGTAGG - AAAAAAAATGATCATGGCAGTGTGTTAGTGGCAATAT	1679
Db	1666	TAGCATTTGCTTACCAAGTAGGAAAAAATGTAATGGCAGTGTGTTAGTGGCAATAT	1725
Qy	1680	AATCTTTGAATTTCTGATTTTTTCAGGCTATAGCTGTATTATCCA - TTTTTTTTACTGT	1738
Db	1726	AATCTTTGAATTTCTGATTTTTTCAGGCTATAGCTGTATTATCCA - TTTTTTTTACTGT	1785
Qy	1739	TATTAAATTTGAACCATAGACTAAGATAAGAACATCATACTATACTGAACACATGT	1798

|||||  
Db 1786 TATTAAATGAAACCATAGACTAAGAAATAAGAAGCATCATACTATAACTGAACACAATGT 1845  
QY 1799 GTATTCATAGTACTGATTTAAATTTCTAAGTGTAACTGAATTAATCATCTGGATTTTT 1858  
|||||  
Db 1846 GTATTCATAGTACTGATTTAAATTTCTAAGTGTAACTGAATTAATCATCTGGATTTTT 1905  
QY 1859 ATTCTTTTCAGATAGGCTTAAACAAATGGAGCTTTCTGTATATAAATGTGGAGATTAGAGT 1918  
|||||  
Db 1906 ATTCTTTTCAGATAGGCTTAAACAAATGGAGCTTTCTGTATATAAATGTGGAGATTAGAGT 1965  
QY 1919 TAATCTCCCAATCACATAATTTGTTTGTGTGAAAAGGAATAAATGTTCCATGCTGG 1978  
|||||  
Db 1966 TAATCTCCCAATCACATAATTTGTTTGTGTGAAAAGGAATAAATGTTCCATGCTGG 2025  
QY 1979 TGGAAAGATAGAGATTGTT 1997  
|||||  
Db 2026 TGGAAAGATAGAGATTGTT 2044  
  
RESULT 12  
E31042  
LOCUS E31042 1659 bp DNA linear PAT 18-JUN-2001  
DEFINITION Method for screening substance inhibiting binding to XIAP.  
ACCESSION E31042  
VERSION E31042.1 GI:13017307  
KEYWORDS JP 1999326328-A/2.  
SOURCE unidentified.  
ORGANISM unclassified.  
  
REFERENCE  
1 (bases 1 to 1659)  
AUTHORS Kunhiro, M.  
TITLE Method for screening substance inhibiting binding to XIAP  
JOURNAL Patent: JP 1999326328-A 2 26-NOV-1999;  
KUNIRO MATSUMOTO  
COMMENT  
OS unidentified  
PN JP 1999326328-A/2  
PD 26-NOV-1999  
PF 13-MAY-1998 JP 1998130378  
PR  
PI KUNIRO MATSUMOTO  
PC G01N33/566,A61K38/00,A61K38/00,A61K38/00,A61K38/22,  
PC A61K39/395,  
PC A61K45/00,A61K45/00,A61K45/00,C07K7/06,C07K7/08,C07K14/47, PC  
G01N33/536,  
PC G01N33/536,G01N33/536//C12N15/09,C12P21/08,A61K37/02,  
A61K37/02, PC A61K37/02,  
PC A61K37/02,A61K37/24,C12N15/00  
CC Strandedness: Double;  
CC Topology: Linear;  
FH Key Location/Qualifiers  
FT CDS 82..1572.  
Location/Qualifiers  
1..1659  
/organism="unidentified"  
/db\_xref="taxon:32644"  
BASE COUNT 519 a 296 c 385 g 459 t  
ORIGIN  
  
Query Match 29.8%; Score 1560; DB 6; Length 1659;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1610; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GAAAGGTGCAGAGTCTCTATTTCAGAGAGAGATGACTTTTACAGTTTGAAGGATCT 60  
|||||  
Db 49 GAAAGGTGCAGAGTCTCTATTTCAGAGAGAGATGACTTTTACAGTTTGAAGGATCT 108  
QY 61 AAAACTTGTCTACCTGCAGACATCAATAAGGAAGAATAATTGPAAGAGATTTAATAGA 120  
|||||  
Db 109 AAACTTGTCTACCTGCAGACATCAATAAGGAAGAATAATTGPAAGAGATTTAATAGA 168  
QY 121 TTAATAAACTTTTGTCTAATTTTCCAAAGTGGTAGTCTCTTTTCAGCATCAACACATGGCACGA 180  
|||||

Db 169 TTAATAAACTTTTGTCTAATTTTCCAAAGTGGTAGTCTCTTTTCAGCATCAACACTGGCACGA 228  
QY 181 GCAGGGTTTCTTTTACTGTTGAAGGAGATACCGTGGGGTCTTTTAGTTGTTCATGCAGCT 240  
|||||  
Db 229 GCAGGGTTTCTTTTACTGTTGAAGGAGATACCGTGGGGTCTTTTAGTTGTTCATGCAGCT 288  
QY 241 GTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAGACACAGAAAGATATCCCCAAAT 300  
|||||  
Db 289 GTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAGACACAGAAAGATATCCCCAAAT 348  
QY 301 TGCAGATTTATCAACGGCTTTTATCTTGAATAATAGTCCCGCAGCTCTACAAATCTCGT 360  
|||||  
Db 349 TGCAGATTTTATCAACGGCTTTTATCTTGAATAATAGTCCCGCAGCTCTACAAATCTCGT 408  
QY 361 ATCCAGAAATGGTCAAGTAAAGTTGAAAACATATCTGGGAAGCAGAGATCATTTTGGCTTTA 420  
|||||  
Db 409 ATCCAGAAATGGTCAAGTAAAGTTGAAAACATATCTGGGAAGCAGAGATCATTTTGGCTTTA 468  
QY 421 GACAGGCCATCTGAGACACATGACAGACTATCTTTTGAGAACTGGCGAGGTTGTAGATATA 480  
|||||  
Db 469 GACAGGCCATCTGAGACACATGACAGACTATCTTTTGAGAACTGGCGAGGTTGTAGATATA 528  
QY 481 TCAGACACCATATATACCCGAGGAACCCCTGCCATGTATAGTGAAGAGCTAGATTTAAAGTCC 540  
Db 529 TCAGACACCATATATACCCGAGGAACCCCTGCCATGTATAGTGAAGAGCTAGATTTAAAGTCC 588  
QY 541 TTTTCAGAACTGGCCAGAGACTATGCTCACTTAACCCCAAGAGAGTTAGCAAGTGCCTGGACTC 600  
|||||  
Db 589 TTTTCAGAACTGGCCAGAGACTATGCTCACTTAACCCCAAGAGAGTTAGCAAGTGCCTGGACTC 648  
QY 601 TACTACACAGTATTTGGTGACCAAGTGCAGTCTTTTGTGGTGGAAAACTGAAAAAT 660  
Db 649 TACTACACAGTATTTGGTGACCAAGTGCAGTCTTTTGTGGTGGAAAACTGAAAAAT 708  
QY 661 TGGGAACCTTGTGATCGTGCCTGTGACAGACACAGGCGACACTTTCCTAAATGCTTCTTT 720  
Db 709 TGGGAACCTTGTGATCGTGCCTGTGACAGACACAGGCGACACTTTCCTAAATGCTTCTTT 768  
QY 721 GTTTTGGGCGGAATCTTAATATTGGAAGTGAATCTGATCTGATGCTGATGATAGGAAT 780  
Db 769 GTTTTGGGCGGAATCTTAATATTGGAAGTGAATCTGATCTGATGCTGATGATAGGAAT 828  
QY 781 TTCCCAAAATTCACAAATCTTTCCAAAGAAATCCATCCATGGCAGATTTATGAAGCAGCGATC 840  
Db 829 TTCCCAAAATTCACAAATCTTTCCAAAGAAATCCATCCATGGCAGATTTATGAAGCAGCGATC 888  
QY 841 TTTTACTTTTGGGACATGGATATACTCAGTTAAACAGGAGCAGCTTGAAGAGCTGGATTT 900  
Db 889 TTTTACTTTTGGGACATGGATATACTCAGTTAAACAGGAGCAGCTTGAAGAGCTGGATTT 948  
QY 901 TATGCTTTTAGTGAAGGTGATAAAGTAAAGTCTTCACTCTGGAGAGGCTTAAGTCTAT 960  
Db 949 TATGCTTTTAGTGAAGGTGATAAAGTAAAGTCTTCACTCTGGAGAGGCTTAAGTCTAT 1008  
QY 961 TGAAGGCCCTAGTGAAGGCCCTTGGGAACAACATGCTAAATGGTATCCAGGTTGCAAAATAT 1020  
Db 1009 TGAAGGCCCTAGTGAAGGCCCTTGGGAACAACATGCTAAATGGTATCCAGGTTGCAAAATAT 1068  
QY 1021 CTGTTAGAACAGAGGAGAACAGAAATATATAAACAAATATTTCAATTAACCTTCACTTGGAG 1080  
Db 1069 CTGTTAGAACAGAGGAGAACAGAAATATATAAACAAATATTTCAATTAACCTTCACTTGGAG 1128  
QY 1081 GAGTGTCTGGTGAAGAACTACTGAGAAACACCATCACTTAACCTAGAGAAATTCATGATACC 1140  
Db 1129 GAGTGTCTGGTGAAGAACTACTGAGAAACACCATCACTTAACCTAGAGAAATTCATGATACC 1188  
QY 1141 ATCTTCCAAATCTCTATGGTACAAAGAGCTATACGAATGGGGTTCAGTTTCAAGGACATTT 1200  
Db 1189 ATCTTCCAAATCTCTATGGTACAAAGAGCTATACGAATGGGGTTCAGTTTCAAGGACATTT 1248  
QY 1201 AAGAAAATTAATGGAGGAAAAAATTCAGATATCTGGGAGCAACTATAAAATCACTTACAGGTT 1260  
Db 1249 AAGAAAATTAATGGAGGAAAAAATTCAGATATCTGGGAGCAACTATAAAATCACTTACAGGTT 1308

```
Qy 1261 CTGGTTCAGATCTAGTGAATGCTCAGAAAGACAGTATGCAAGATGAGTCAAGTCAGACT 1320
Db 1309 CTGGTTCAGATCTAGTGAATGCTCAGAAAGACAGTATGCAAGATGAGTCAAGTCAGACT 1368
Qy 1321 TCATTACAGAAGAGATTAGTACTGAAGACAGAGTAAAGCGCCTGCAAGAGAGAAAGCTT 1380
Db 1369 TCATTACAGAAGAGATTAGTACTGAAGACAGAGTAAAGCGCCTGCAAGAGAGAAAGCTT 1428
Qy 1381 TGCAAAATCTGTATGGATAGAAATATTGCTATCGTTTGTGTTTCTGTTGGACATCTAGTC 1440
Db 1429 TGCAAAATCTGTATGGATAGAAATATTGCTATCGTTTGTGTTTCTGTTGGACATCTAGTC 1488
Qy 1441 ACTTGTAACAATGTGCTGAAGCAGTGTGACAAGTGTCCCATGTGCTACACAGTCAATTACT 1500
Db 1489 ACTTGTAACAATGTGCTGAAGCAGTGTGACAAGTGTCCCATGTGCTACACAGTCAATTACT 1548
Qy 1501 TTCAGCAAAAATTTTATGCTCTAAATCTAACTCTATAGTAGGATGTTATGTTGTTCT 1560
Db 1549 TTCAGCAAAAATTTTATGCTCTAAATCTAACTCTATAGTAGGATGTTATGTTGTTCT 1608
Qy 1561 TATTACCCCTGATTGAATGTGATGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1611
Db 1609 TATTACCCCTGATTGAATGTGATGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1659

RESULT 13
HSU32974      1659 bp      mRNA      linear      PRI 12-JUN-1996
LOCUS      Human IAP-like protein ILP mRNA, complete cds.
DEFINITION      U32974
ACCESSION      U32974
VERSION      1 GI:1016687
KEYWORDS      apoptosis; ring finger; zinc finger.
SOURCE      Homo sapiens.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Duckett,C.S., Nava,V.E., Gedrich,R.W., Clem,R.J., Van Dongen,J.L.,
Gilfillan,M.C., Shiels,H., Hardwick,J.M. and Thompson,C.B.
A conserved family of cellular genes related to the baculovirus iap
gene and encoding apoptosis inhibitors
EMBO J. 15 (11), 2685-2694 (1996)
96256286
PUBMED      8654366
REFERENCE      2 (bases 1 to 1659)
Duckett,C.S. and Thompson,C.B.
Direct Submission
AUTHORS
TITLE      Submitted (01-AUG-1995) Colin Duckett, Howard Hughes Medical
Institute, The University of Chicago, 924 East 57th Street,
Chicago, IL 60637, USA
JOURNAL
FEATURES
source      Location/Qualifiers
1..1659
/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="heart"
/clone_lib="lambda gt10, Clontech Laboratories, Cat number
HL3018a"
/dev_stage="fetus"
82..1575
/codon_start=1
/product="IAP-like protein ILP"
/protein_id="AAC50518.1"
/db_xref="GI:1016688"
translation="MTNSEGSKTCVPADINKKEEVEEFENRLKTFANFPSSPVSA
STLARGFLTYGEGDVRCSFHAADVGRHRRKVPNCRFNGFYLENSA
TQNSNGIQGVKYNLGRSDHFDALDRPETHADYLLRGTQGVVDLSDIYPRNPAM
YSEARLKSNQNPDPYLAHLPRELASGLAYTIGDQVQCFCGCGKLKNWPCDRAWS
EHRHFFNCFEVLGNLNIRESDAVSSDRNFNSTLPRNPMSADYEARELFTFTWI
YSVNKEOLAFVAGLEGDKVKCFHCGGGITDWPSEDPKQEHAKWPKCKVILEOK
GOEYINNIHLTHSLECLVTRTEKTPSLTRIDDTIFQNPWVQFAIRMGFSFKDIKI
MEEKIQLSGNNYSLEVLVADLVNAQKSDPDESSQTSLOKEISTEQLRRLOEKLK
KICMDRNIATVFPVCGHLVTCQCAEAADVRCPCMYTIVTFKQIFMS"
```

```
misc_feature      163..363
/note="IAP repeat"
misc_feature      574..774
/note="IAP repeat"
misc_feature      877..1068
/note="IAP repeat"
misc_feature      1420..1542
/note="RING finger"
BASE COUNT      519 a      296 c      459 t
ORIGIN
Query Match      29.8%; Score 1560; DB 9; Length 1659;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1610; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GAAAGAGTGGACAAGTCTCTATTTTCAAGAGAGAGATGACTTTTAAACAGTTTTCGAAGSATCT 60
Db 49 GAAAGAGTGGACAAGTCTCTATTTTCAAGAGAGAGATGACTTTTAAACAGTTTTCGAAGSATCT 108
Qy 61 AAAACTTGTGTACCTGCAGACATCAATAAGGAAGAAGAAATTTGTAGAAGAGTTTAATAGA 120
Db 109 AAAACTTGTGTACCTGCAGACATCAATAAGGAAGAAGAAATTTGTAGAAGAGTTTAATAGA 168
Qy 121 TTAATAAATTTTGTCTAATTTTCCAAAGTGGTAGTCTCTGTTTCAGCATCAACACTGGCAGCA 180
Db 169 TTAATAAATTTTGTCTAATTTTCCAAAGTGGTAGTCTCTGTTTCAGCATCAACACTGGCAGCA 228
Qy 181 CGAGGGTTTCTTATACCTGGTGAAGAGATACCGTGCCTGCTTTAGTTGTCATCAGCT 240
Db 229 CGAGGGTTTCTTATACCTGGTGAAGAGATACCGTGCCTGCTTTAGTTGTCATCAGCT 288
Qy 241 GTAGATAGATGCAATATGGAGACTCAGCAGTGTGGAAGACACAGAGAAAGTATCCCAAT 300
Db 289 GTAGATAGATGCAATATGGAGACTCAGCAGTGTGGAAGACACAGAGAAAGTATCCCAAT 348
Qy 301 TGCAGATTTATCAACGGCTTTTATCTTGAAATATGTCGACGATGTACAAATTTCTGGT 360
Db 349 TGCAGATTTATCAACGGCTTTTATCTTGAAATATGTCGACGATGTACAAATTTCTGGT 408
Qy 361 ATCCAGAAATGGTCACTACAAAGTTGAAACATCTCTGGAAGCAGAGATCATTTTCCCTTA 420
Db 409 ATCCAGAAATGGTCACTACAAAGTTGAAACATCTCTGGAAGCAGAGATCATTTTCCCTTA 468
Qy 421 GACAGGCCATCTGAGACACATCGACAGTATCTTTTGAACATGGCGAGTTGTAGATATA 480
Db 469 GACAGGCCATCTGAGACACATCGACAGTATCTTTTGAACATGGCGAGTTGTAGATATA 528
Qy 481 TCAGACACCATATACCCGAGGACCCCTGCCATGTATAGTGAAGAAGCTAGATTAAAGTCC 540
Db 529 TCAGACACCATATACCCGAGGACCCCTGCCATGTATAGTGAAGAAGCTAGATTAAAGTCC 588
Qy 541 TTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTCTCGACTC 600
Db 589 TTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTCTCGACTC 648
Qy 601 TACTACAGAGTATTGGTGACCAAGTGCAGTCTTTTGTGTTGGTGGAAAACTGAAAAAT 660
Db 649 TACTACAGAGTATTGGTGACCAAGTGCAGTCTTTTGTGTTGGTGGAAAACTGAAAAAT 708
Qy 661 TGGGAACCTTGTGATGTGCGCTGTGTCAGAACACAGCGGACACTTTCCCTAAATGCTCTTT 720
Db 709 TGGGAACCTTGTGATGTGCGCTGTGTCAGAACACAGCGGACACTTTCCCTAAATGCTCTTT 768
Qy 721 GTTTGGGCCCGAATCTTAAATTCGAAGTGAATCTGATGCTGTCAGTTCGATAGGAAT 780
Db 769 GTTTGGGCCCGAATCTTAAATTCGAAGTGAATCTGATGCTGTCAGTTCGATAGGAAT 828
Qy 781 TTCCCAAAATCAACAAATCTTCCAAAGAAATCCATCCATGGCAGATTTATGAAGCAGCGATC 840
Db 829 TTCCCAAAATCAACAAATCTTCCAAAGAAATCCATCCATGGCAGATTTATGAAGCAGCGATC 888
Qy 841 TTTTACTTTTGGACATGGATATACCTAGTTTAAACAGAGAGAGCTTTGCAAGAGCTGGATTT 900
Db 841 TTTTACTTTTGGACATGGATATACCTAGTTTAAACAGAGAGAGCTTTGCAAGAGCTGGATTT
```



```
Db 889 TTTACTTTTGGGACATGGATATATCTAGTTAAACAAGGAGGAGCTTGCAAGAGCTGGATT 948
QY 901 TATGCTTTAGTGTGAAGTGATATAAGTAAAGTCTTTTCTGCTGAGGAGGCTAACTGAT 960
Db 949 TATGCTTTAGTGTGAAGTGATATAAGTAAAGTCTTTTCTGCTGAGGAGGCTAACTGAT 1008
QY 961 TGAAGCCCAAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGCTGCAAAATAT 1020
Db 1009 TGAAGCCCAAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGCTGCAAAATAT 1068
QY 1021 CTGTTAGAACAGGAGGACAGATATATATAACAATATTTTAACTCATTTGAG 1080
Db 1069 CTGTTAGAACAGGAGGACAGATATATAACAATATTTTAACTCATTTGAG 1128
QY 1081 GAGTGTCTGCTAGAACCTACTGAGAAACACCATCACTAACTAGCAAAATTTGATGATACC 1140
Db 1129 GAGTGTCTGCTAGAACCTACTGAGAAACACCATCACTAACTAGCAAAATTTGATGATACC 1188
QY 1141 ATCTTCAAAATCCTATGTTGACAAAGAGCTATACGAATGGGGTTCAGTTTCAAGGACATT 1200
Db 1189 ATCTTCAAAATCCTATGTTGACAAAGAGCTATACGAATGGGGTTCAGTTTCAAGGACATT 1248
QY 1201 AAGAAATATAGGAGGAAAAATTCAGATATCTGGGAGCACTATAAATCACTTGAGGTT 1260
Db 1249 AAGAAATATAGGAGGAAAAATTCAGATATCTGGGAGCACTATAAATCACTTGAGGTT 1308
QY 1261 CTGTTTCAGATCTAGTGAATGCTCAGAAAGACAGATATGCAAGATGAGTCAAGTCAGACT 1320
Db 1309 CTGTTTCAGATCTAGTGAATGCTCAGAAAGACAGATATGCAAGATGAGTCAAGTCAGACT 1368
QY 1321 TCATTACAGAAAGAGATTAGTACTGAAAGACAGCTAAAGGCGCCCTGCAAGAGGAGGAAGCTT 1380
Db 1369 TCATTACAGAAAGAGATTAGTACTGAAAGACAGCTAAAGGCGCCCTGCAAGAGGAGGAAGCTT 1428
QY 1381 TGCAAATCTGTATGGATAGAAATATTTGCTATCGTTTTTGTCTTGTGACATCTAGTC 1440
Db 1429 TGCAAATCTGTATGGATAGAAATATTTGCTATCGTTTTTGTCTTGTGACATCTAGTC 1488
QY 1441 ACTTGTAAACATGCTGTAAGCAGTTGCAAGTGCTCCCATGTGCTACACAGTCATTAAT 1500
Db 1489 ACTTGTAAACATGCTGTAAGCAGTTGCAAGTGCTCCCATGTGCTACACAGTCATTAAT 1548
QY 1501 TTCAAGCAAAAAATTTTATGCTTAACTTAATCTATAGTAGGCATGTTATGTTGTTCT 1560
Db 1549 TTCAAGCAAAAAATTTTATGCTTAACTTAATCTATAGTAGGCATGTTATGTTGTTCT 1608
QY 1561 TATTACCTCATGAATGTGTGATGCTGAACCTGACTTTAAGTAATCAGGATT 1611
Db 1609 TATTACCTCATGAATGTGTGATGCTGAACCTGACTTTAAGTAATCAGGATT 1659

RESULT 14
HS424J12
LOCUS HS424J12
DEFINITION Homo sapiens chromosome X clone RP3-424J12, *** SEQUENCING IN
PROGRESS ***, 15 unordered pieces.
ACCESSION 282207
VERSION 282207.3 GI:12331276
KEYWORDS HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 201197)
Grafham.D.
Direct Submission
Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Jan 22, 2001 this sequence version replaced gi:10045116.
----- Genome Center
Center: Sanger Centre
Center code: SC
```

```
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: DJ424J12
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M7815; 74% of reads
Sequencing vector: plasmid; 108752; 25% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Chemistry: Dye-terminator ABI; 96% of reads
Chemistry: Dye-terminator-amersham; 2% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Consensus quality: 194333 bases at least Q40
Consensus quality: 196512 bases at least Q30
Consensus quality: 198047 bases at least Q20
Insert size: 199797; sum-of-contigs
Quality coverage: 6.87x in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 4154: contig of 4154 bp in length
* 4155 4254: gap of 100 bp
* 4255 18703: contig of 14449 bp in length
* 18704 18803: gap of 100 bp
* 18804 20941: contig of 2138 bp in length
* 20942 21041: gap of 100 bp
* 21042 34907: contig of 13866 bp in length
* 34908 35012: gap of 105 bp
* 35013 37508: contig of 2496 bp in length
* 37509 37608: gap of 100 bp
* 37609 52739: contig of 15131 bp in length
* 52740 52839: gap of 100 bp
* 52840 56933: contig of 4094 bp in length
* 56934 57033: gap of 100 bp
* 57034 88245: contig of 31212 bp in length
* 88246 88346: gap of 101 bp
* 88347 93386: contig of 5040 bp in length
* 93387 93486: gap of 100 bp
* 93487 123956: contig of 30470 bp in length
* 123957 124056: gap of 100 bp
* 124057 147917: contig of 23861 bp in length
* 147918 148017: gap of 100 bp
* 148018 176236: contig of 28219 bp in length
* 176237 176336: gap of 100 bp
* 176337 187128: contig of 10792 bp in length
* 187129 187228: gap of 100 bp
* 187229 190824: contig of 3596 bp in length
* 190825 190959: gap of 135 bp
* 190960 201197: contig of 10238 bp in length.
FEATURES
Location/Qualifiers
1..201197
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
/clone="RP3-424J12"
/clone_lib="RPCI-3"
1..4154
/notes="assembly_fragment:02486
fragment_chain:1"
misc_feature
1..4154
/notes="assembly_fragment:04764
fragment_chain:1"
misc_feature
18804..20941
/notes="assembly_fragment:03282
fragment_chain:2"
misc_feature
21042..34907
/notes="assembly_fragment:03624
fragment_chain:3"
```



Qy

sequence. The true right end of clone RP11-402N18 is at 2000 in this sequence.

FEATURES  
source  
Location/Qualifiers  
1..158093  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="10"  
/clone="RP11-566F5"  
/clone\_lib="RPCI-11.2"  
BASE COUNT 49096 a 31903 c 31075 g 46019 t  
ORIGIN

Query Match 2.88; Score 146; DB 9; Length 158093;  
Best Local Similarity 99.2%; Pred. No. 3.4e-61;  
Matches 246; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 926 TAAAGTGCTTTCACGTGGAGGGGCTAACTGATTGGAGCCCGCCAGTCAAGACCCCTTGGG 985  
DB 88645 TAAAGTGCTTTCACGTGGAGGGGCTAACTGATTGGAGCCCGCCAGTCAAGACCCCTTGGG 88704  
QY 986 AACACATGCTAAATGGTATCCAGGGTGCAAAATATCTGTAGAACAGAGGCAAGAAT 1045  
DB 88705 AACACATGCTAAATGGTATCCAGGGTGTAATATCTGTAGAACAGAGGCAAGAAT 88764  
QY 1046 ATATAACAATATTCATTTAACTCACTTGAGGAGTGCTGTAGAACAGAGGCAAGAAT 1105  
DB 88765 ATATAACAATATTCATTTAACTCACTTGAGGAGTGCTGTAGAACAGAGGCAAGAAT 88824  
QY 1106 AACACCATCACTAAGTAGAAGATTGATGATACCATCTTCCAAAATCCTATGTTACAAG 1165  
DB 88825 AACACCATCACTAAGTAGAAGATTGATGATACCATCTTCCAAAATCCTATGTTACAAG 88884  
QY 1166 AAGCTATA 1173  
DB 88885 AAGCTATA 88892

Search completed: November 10, 2002, 00:05:51  
Job time : 14443 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 9, 2002, 19:41:40 ; Search time 964 seconds

(without alignments)  
12222.464 Million cell updates/sec

Title: US-09-974-592-3

Perfect score: 5232

Sequence: 1 gaaaggtggaagtctcta.....tcaaaaaaaaaaaaaaaag 5232

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_101002.\*

- 1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.\*
- 2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.\*
- 3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.\*
- 4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.\*
- 5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.\*
- 6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.\*
- 7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.\*
- 8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.\*
- 9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.\*
- 10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.\*
- 11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.\*
- 12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.\*
- 13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.\*
- 14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.\*
- 15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.\*
- 16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.\*
- 17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.\*
- 18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.\*
- 19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.\*
- 20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.\*
- 21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.\*
- 22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.\*
- 23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.\*
- 24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5232	100.0	5232	19 AAV55038	Human XIAP coding
2	2511	48.0	8763	22 AAK89468	Human digestive sy
3	2278	43.5	3000	24 AAK93875	Human cDNA encodin
4	2027	38.7	2404	24 AAK99405	DNA of APP related
5	1990	38.0	2540	18 AAT70836	Human apoptosis in
6	1990	38.0	2540	21 AAA64901	Human x-linked inh
7	1969	37.6	2540	24 AAK93869	Human cDNA encodin
8	1560	29.8	1659	21 AAZ48862	Human XIAP coding
9	469	9.0	469	22 AAK89469	Human digestive sy

c 10	466	8.9	489	22	ABA43584	Human breast cell
c 11	466	8.9	489	22	AAI12335	Probe #2268 for ge
c 12	466	8.9	489	22	AAI02249	Probe #2240 used t
c 13	359	6.9	417	22	AAH33140	Human colon cancer
c 14	314	6.0	315	21	AAC23231	Human secreted pro
c 15	202	3.9	1129	22	AAH99222	Human protein enco
c 16	198	3.8	1533	23	AAH74582	DNA encoding novel
c 17	198	3.8	1533	23	AAH88274	DNA encoding novel
c 18	151	2.9	190	21	AAC24217	Human secreted pro
c 19	148	2.8	148	22	ABA48694	Human breast cell
c 20	148	2.8	148	22	AAI21530	Probe #11463 for g
c 21	148	2.8	148	22	AAI07226	Probe #7217 used t
c 22	131	2.5	302	24	ABQ58785	Human colon cancer
c 23	103	2.0	40328	21	AAZ92584	Human DAZ genomic
c 24	103	2.0	43795	21	AAZ92583	Human DAZ genomic
c 25	101	1.9	160552	22	AAD02697	Human glycosyl sul
c 26	97	1.9	7885	22	AAK70210	Human immune/haema
c 27	89	1.7	194	22	AAI36061	Human musculoskele
c 28	87	1.7	140036	24	AAH98600	Human genomic DNA
c 29	85	1.6	237	21	AAC21919	Human secreted pro
c 30	85	1.6	4274	22	AAK67096	Human immune/haema
c 31	85	1.6	5076	22	ABAI6699	Human nervous syst
c 32	85	1.6	5332	22	AAH30405	DNA encoding novel
c 33	85	1.6	5332	22	AAI04432	Human reproductive
c 34	85	1.6	5372	22	AAH30406	DNA encoding novel
c 35	85	1.6	5372	22	AAI04433	Human reproductive
c 36	85	1.6	6352	22	AAH30407	DNA encoding novel
c 37	85	1.6	6352	22	AAI04434	Human reproductive
c 38	85	1.6	48203	22	AAK70161	Human immune/haema
c 39	85	1.6	48203	22	AAK81663	Human immune/haema
c 40	85	1.6	48203	22	AAK82628	Human immune/haema
c 41	85	1.6	48204	22	AAK70164	Human immune/haema
c 42	85	1.6	48204	22	AAK81666	Human immune/haema
c 43	85	1.6	48204	22	AAK82630	Human immune/haema
c 44	85	1.6	53552	22	AAH36555	Genomic DNA sequen
c 45	85	1.6	222930	24	ABK84349	Human cDNA differe

ALIGNMENTS

RESULT 1

AAV55038

ID AAV55038 standard; cDNA; 5232 BP.

XX AAV55038;

XX 13-NOV-1998 (first entry)

DT Human XIAP coding sequence.

DE Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;  
KW proliferative disease; IAP; therapy; cancer; human; XIAP protein; ss.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 34..1527

FT /\*tag= a

FT /product= XIAP

XX WO9835693-A2.

XX 20-AUG-1998.

XX 13-FEB-1998; 98WO-IB00781.

XX 13-FEB-1997; 97US-0800929.

XX (UYOT-) UNIV OTTAWA.

XX Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;

XX Tsang B;

XX WPI; 1998-467164/40.  
DR P-PSDB; AAW69294.  
XX  
PT Inducing apoptosis in proliferative mammalian cells with inhibitor  
PT of IAP or NAIP polypeptide - also methods for prognosis based on  
PT presence of IAP and NAIP, specifically applied to cancers involving  
PT p53 mutations  
XX  
PS Claim 13; Fig 1; 147pp; English.  
XX  
CC This sequence encodes the human XIAP protein, which is a inhibitor of  
CC apoptosis protein (IAP), and can be used in the method of the invention.  
CC The method is for enhancing apoptosis in cells from a mammal with  
CC proliferative disease by treatment with a compound that inhibits  
CC biological activity of an IAP or NAIP polypeptide. The inhibitory  
CC compounds are used to treat proliferative diseases, specially cancers of  
CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,  
CC liver, nasopharynx, thyroid, central nervous system, prostate, colon,  
CC rectum, cervix or endometrium, particularly to increase their sensitivity  
CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are  
CC detected in many cancers and are associated with poor prognosis,  
CC resistance to chemotherapeutic agents and mutations in p53 (it is  
CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP  
CC genes). Transgenic animals are used for testing the effects of antisense  
CC oligonucleotides and for screening for the inhibitors.  
XX  
SQ Sequence 5232 BP; 1579 A; 861 C; 1062 G; 1728 T; 2 other;

QY 601 TACTACACAGGTATGGTGACCAAGTCAGATGCTTTTGTGGTGGAAAACTGAAAAAT 660  
DB TACTACACAGGTATGGTGACCAAGTCAGATGCTTTTGTGGTGGAAAACTGAAAAAT 660  
QY 661 TGGNAACCTTGTGATCGTCCGTGTCAGAACACAGGCGACACTTTCCTAAATGCTCTTT 720  
DB TGGNAACCTTGTGATCGTCCGTGTCAGAACACAGGCGACACTTTCCTAAATGCTCTTT 720  
QY 721 GTTTTGGGCGGAATCTTAATATTGGAAGTGAATCTGATGCTGCTGATGATAGGAAT 780  
DB GTTTTGGGCGGAATCTTAATATTGGAAGTGAATCTGATGCTGATGATAGGAAT 780  
QY 781 TTCCCAATTCACCAAAATCTTCCAAAGAAATCCATCCATGGCAGATATGAAGCAGGATC 840  
DB TTCCCAATTCACCAAAATCTTCCAAAGAAATCCATCCATGGCAGATATGAAGCAGGATC 840  
QY 841 TTTACTTTTGGGACATGGATATCTCAGTTAACAGGAGCAGCTTGCAGAGCTGGATTT 900  
DB TTTACTTTTGGGACATGGATATCTCAGTTAACAGGAGCAGCTTGCAGAGCTGGATTT 900  
QY 901 TATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGAGGAGGCTAACTCAT 960  
DB TATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGAGGAGGCTAACTCAT 960  
QY 961 TGGAAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCAATPAT 1020  
DB TGGAAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCAATPAT 1020  
QY 1021 CTGTTAGNACAGAGGGACAAAGATATATAAACAATATTCATTTAACTCATCTTCTGAG 1080  
DB CTGTTAGNACAGAGGGACAAAGATATATAAACAATATTCATTTAACTCATCTTCTGAG 1080  
QY 1081 GAGTGTCTGGTGAAGAACTTACTGAGAAAAACACCATCACTAAGTAAAGTATGATGATACC 1140  
DB GAGTGTCTGGTGAAGAACTTACTGAGAAAAACACCATCACTAAGTAAAGTATGATGATACC 1140  
QY 1141 ATCTTCCAAAATCCTATGGTACAAAGAGCTATACGAATGGGGTTCAGTTTCAAGGACACT 1200  
DB ATCTTCCAAAATCCTATGGTACAAAGAGCTATACGAATGGGGTTCAGTTTCAAGGACACT 1200  
QY 1201 AAGAAAATAATGGAGGAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTGAAGTT 1260  
DB AAGAAAATAATGGAGGAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTGAAGTT 1260  
QY 1261 CTGGTTGCAGATCTAGTGAATGCTCAGAAAAGACAGTATGCAAGATGAGTCAAGTCAAGT 1320  
DB CTGGTTGCAGATCTAGTGAATGCTCAGAAAAGACAGTATGCAAGATGAGTCAAGTCAAGT 1320  
QY 1321 TCATTACAGAAAGAGATTAGTACTGCAAGAGCTAAGCGCGCTGCAAGAGAGAGAGCTT 1380  
DB TCATTACAGAAAGAGATTAGTACTGCAAGAGCTAAGCGCGCTGCAAGAGAGAGAGCTT 1380  
QY 1381 TGCAAAATCTCTATGGATAGAAATATTCGTATCTGTTTGTCTTGTGGACATCTAGTC 1440  
DB TGCAAAATCTCTATGGATAGAAATATTCGTATCTGTTTGTCTTGTGGACATCTAGTC 1440  
QY 1441 ACTTGTAAACAATGTGCTGAAGCAGCTGACAAAGTGTCCCATGTGCTACACAGTCAATTACT 1500  
DB ACTTGTAAACAATGTGCTGAAGCAGCTGACAAAGTGTCCCATGTGCTACACAGTCAATTACT 1500  
QY 1501 TTCAAGCAAAAAATTTTATCTCTTAATCTAATCTATAGTAGGAGCTGTTATGTTGTTCT 1560  
DB TTCAAGCAAAAAATTTTATCTCTTAATCTAATCTATAGTAGGAGCTGTTATGTTGTTCT 1560  
QY 1561 TATTACCTGATTAAGTGTGATGTAAGTGAACCTGACTTTAAGTAATCAGGATTAATTCAT 1620  
DB TATTACCTGATTAAGTGTGATGTAAGTGAACCTGACTTTAAGTAATCAGGATTAATTCAT 1620  
QY 1621 TAGCATTTGCTACCAAGTAGGAAAAAATGTACATGTCAGTGTGTTTGTAGTTGGCAATATA 1680  
DB TAGCATTTGCTACCAAGTAGGAAAAAATGTACATGTCAGTGTGTTTGTAGTTGGCAATATA 1680  
QY 1681 ATCTTTGAATTTCTTGATTTTTCAGGGTATATAGCTGTATATTCATTTTTTTTACTGTATA 1740

Db 1681 ATCTTTGAAATTTCTTGATTTTTCAGGGTATTAGCTGTATTATCCATTTTTFCTACTGTTA 1740  
QY TTTAAATGAAACCATAGACTAAGAATAAGAACGATCATACTATAACTGAAACACAATGTGT 1800  
Db 1741 TTTAAATGAAACCATAGACTAAGAATAAGAACGATCATACTATAACTGAAACACAATGTGT 1800  
QY ATTCATAGTATCTGATTTAAATTTCTTAAGTGTAAAGTGAATTAATCATCTCGATTTTAT 1860  
Db 1801 ATTCATAGTATCTGATTTAAATTTCTTAAGTGTAAAGTGAATTAATCATCTCGATTTTAT 1860  
QY TCCTTTTCAGATAGGCTTAACAATGAGCTTCTGTATATAAATGTCGAGATTAGAGTTA 1920  
Db 1861 TCCTTTTCAGATAGGCTTAACAATGAGCTTCTGTATATAAATGTCGAGATTAGAGTTA 1920  
QY ATCTCCCAATACATAATTTGTTGTGGAAGAGGAATAAATGTTCCATGCTGGTG 1980  
Db 1921 ATCTCCCAATACATAATTTGTTGTGGAAGAGGAATAAATGTTCCATGCTGGTG 1980  
QY 1981 GAAAGATAGAGATTGTTTTAGAGTTGGTGTGTTTTAGGATCTGTCCATTTCT 2040  
Db 1981 GAAAGATAGAGATTGTTTTAGAGTTGGTGTGTTTTAGGATCTGTCCATTTCT 2040  
QY TTTAAAGTTATAACACGCTACTTGTGCGAATTTATTTTTTAAAGTGATTTGCCATTTTG 2100  
Db 2041 TTTAAAGTTATAACACGCTACTTGTGCGAATTTATTTTTTAAAGTGATTTGCCATTTTG 2100  
QY AAAGCGTATTTAATGATAGATACTATCGAGCCAAACATGTGACATGGAAGAGTCA 2160  
Db 2101 AAAGCGTATTTAATGATAGATACTATCGAGCCAAACATGTGACATGGAAGAGTCA 2160  
QY 2161 AAGATATGTTAAAGTAAATGCAAGTGGCAAAACACTATGTAGTCTGAGCCAGATCA 2220  
Db 2161 AAGATATGTTAAAGTAAATGCAAGTGGCAAAACACTATGTAGTCTGAGCCAGATCA 2220  
QY 2221 AAGTATGATGTTTTTAATGATAGATAGAACAAAGATTTGGAAGATATACAAACTG 2280  
Db 2221 AAGTATGATGTTTTTAATGATAGATAGAACAAAGATTTGGAAGATATACAAACTG 2280  
QY TTAATATGTTGTTCTCTCGGGGAGGGGGGATTTGGGGAGGGGCCCCAGAGGGTTTTA 2340  
Db 2281 TTAATATGTTGTTCTCTCGGGGAGGGGGGATTTGGGGAGGGGCCCCAGAGGGTTTTA 2340  
QY 2341 TAGGGGCTTTTCACCTTTCTACCTTTTTCATTTTGTCTGTCGAATTTTATAAGTAT 2400  
Db 2341 TAGGGGCTTTTCACCTTTCTACCTTTTTCATTTTGTCTGTCGAATTTTATAAGTAT 2400  
QY 2401 GTATTACTTTTGTAAATCAGAAATTTTGAAGATATTTTGTCTGATTTAAAGCTTAGGCAT 2460  
Db 2401 GTATTACTTTTGTAAATCAGAAATTTTGAAGATATTTTGTCTGATTTAAAGCTTAGGCAT 2460  
QY 2461 GTTCAACGCTCGCAAACTTATACCTACCTACCTAGCTTTAGTTTCTTAATCCAAAGGCA 2520  
Db 2461 GTTCAACGCTCGCAAACTTATACCTACCTACCTAGCTTTAGTTTCTTAATCCAAAGGCA 2520  
QY 2521 GGGCAGTTAACCTTTTGTGTGCAATGTGAAATGTAAATGATTTATGTTTTTCTGCTT 2580  
Db 2521 GGGCAGTTAACCTTTTGTGTGCAATGTGAAATGTAAATGATTTATGTTTTTCTGCTT 2580  
QY 2581 TGTGGATGAAAAATATTTCTGAGTGGTGTGTTTTTGTACAGGTAGACCATGCTTTATCTTG 2640  
Db 2581 TGTGGATGAAAAATATTTCTGAGTGGTGTGTTTTTGTACAGGTAGACCATGCTTTATCTTG 2640  
QY 2641 TTTCAAAATAGATTTCTGATTTTGTAAATGAATATATAAATATGCTCAGATCTTCC 2700  
Db 2641 TTTCAAAATAGATTTCTGATTTTGTAAATGAATATATAAATATGCTCAGATCTTCC 2700  
QY 2701 AATTAATTAGTAGGATTCATCTTAAATCCTTCTGCTAGTTTAAAGCTGCTTAAGTCACTT 2760  
Db 2701 AATTAATTAGTAGGATTCATCTTAAATCCTTCTGCTAGTTTAAAGCTGCTTAAGTCACTT 2760  
QY 2761 ACTAAAAGATCTTTGTTAACTCAGTATTTTAAACATCTGTCAGCTTATGTAGTAAAGT 2820

Db 2761 ACTAAAAGATCTTTGTTAACTCAGTATTTTAAACATCTGTCAGCTTATGTAGTAAAAAGT 2820  
QY 2821 AGAAGCATGTTTGTACACTGCTTGTAGTTATAGTGACAGCTTTCCATGTTGAGATTTCTCA 2880  
Db 2821 AGAAGCATGTTTGTACACTGCTTGTAGTTATAGTGACAGCTTTCCATGTTGAGATTTCTCA 2880  
QY 2881 TATCATCTTGTATCTCTTAAAGTTTTCATGTAGTTTTCACCGTTAGGATGATTAAAGATGAT 2940  
Db 2881 TATCATCTTGTATCTCTTAAAGTTTTCATGTAGTTTTCACCGTTAGGATGATTAAAGATGAT 2940  
QY 2941 ATAGGCAAAATCTTAAAGTTTTCATGTAGTTTTCACCGTTAGGATGATTAAAGATGAT 3000  
Db 2941 ATAGGCAAAATCTTAAAGTTTTCATGTAGTTTTCACCGTTAGGATGATTAAAGATGAT 3000  
QY 3001 GTAGATCTTCTGAAATATAATGTTCTCAAGATCTTAAACCTCTTGAAAAATATAAA 3060  
Db 3001 GTAGATCTTCTGAAATATAATGTTCTCAAGATCTTAAACCTCTTGAAAAATATAAA 3060  
QY 3061 AATATTGGCAAGAAAAAGAAATAGTTGTTTAAATATTTTTTAAAAAACAACCTTGAATAAG 3120  
Db 3061 AATATTGGCAAGAAAAAGAAATAGTTGTTTAAATATTTTTTAAAAAACAACCTTGAATAAG 3120  
QY 3121 AATCAGTAGGGTATAAATAGAAAGTTTAAATGCTCATAGAACGTCAGGGTTTACAT 3180  
Db 3121 AATCAGTAGGGTATAAATAGAAAGTTTAAATGCTCATAGAACGTCAGGGTTTACAT 3180  
QY 3181 TACAAGATTTCTCAACAACCCCATTTGTAGAGTGTAGTAAAGGATGTTACTACAGAGAA 3240  
Db 3181 TACAAGATTTCTCAACAACCCCATTTGTAGAGTGTAGTAAAGGATGTTACTACAGAGAA 3240  
QY 3241 AGTTTGAGAGTAAACCTGTAATAATTTATTTTTTGTGTACTTTCTTAAGAGAAAGAGTA 3300  
Db 3241 AGTTTGAGAGTAAACCTGTAATAATTTATTTTTTGTGTACTTTCTTAAGAGAAAGAGTA 3300  
QY 3301 TTGTTATGTTCTCCTAACTTCTGTTGATTAATTTTAAAGTGATTTTCAATTTAAACATTT 3360  
Db 3301 TTGTTATGTTCTCCTAACTTCTGTTGATTAATTTTAAAGTGATTTTCAATTTAAACATTT 3360  
QY 3361 GCAAAATTAATTTATTTTAAATTTTCTTTTGTAGATGAGTCTGCTGTGTACCCAGG 3420  
Db 3361 GCAAAATTAATTTATTTTAAATTTTCTTTTGTAGATGAGTCTGCTGTGTACCCAGG 3420  
QY 3421 CTGAGTGTGAGTGTGATCTCTGCTCACTGCAACCTCCGCCCTTCTGGGTTCAAGCAT 3480  
Db 3421 CTGAGTGTGAGTGTGATCTCTGCTCACTGCAACCTCCGCCCTTCTGGGTTCAAGCAT 3480  
QY 3481 TCTCGGCCCTCAGCTTCTCTGAGTGTGGAATTTACAGGAGGTCGCCACCATGCCGACTA 3540  
Db 3481 TCTCGGCCCTCAGCTTCTCTGAGTGTGGAATTTACAGGAGGTCGCCACCATGCCGACTA 3540  
QY 3541 ATTTTTTTTTTATTTTATAGTAGAGACGGGTTTTCACCATGTTGGCCAGGCTGGTATCAAC 3600  
Db 3541 ATTTTTTTTTTATTTTATAGTAGAGACGGGTTTTCACCATGTTGGCCAGGCTGGTATCAAC 3600  
QY 3601 TCCTGACCTCAAGAGATCCACTCGCCCTTGCCCTCCCAAGTGTCTGGGATTTACAGGCTTGA 3660  
Db 3601 TCCTGACCTCAAGAGATCCACTCGCCCTTGCCCTCCCAAGTGTCTGGGATTTACAGGCTTGA 3660  
QY 3661 GGCACACGCCCCGGCTAAACATTTGCAAAATTTAAATGAGAGTTTTAAAAATTTAAATATG 3720  
Db 3661 GGCACACGCCCCGGCTAAACATTTGCAAAATTTAAATGAGAGTTTTAAAAATTTAAATATG 3720  
QY 3721 ACTGCCCTGTTTCTGTTTTAGTATGTAATCTCAGTTCTTCACTTTTGACCTGTCTGCC 3780  
Db 3721 ACTGCCCTGTTTCTGTTTTAGTATGTAATCTCAGTTCTTCACTTTTGACCTGTCTGCC 3780  
QY 3781 ACTTAGTTTGGTTATATAGTCATTAACTTGAATTTTGTCTGTATAGTCTAGACTTTAAAT 3840  
Db 3781 ACTTAGTTTGGTTATATAGTCATTAACTTGAATTTTGTCTGTATAGTCTAGACTTTAAAT 3840  
QY 3841 TTAAGTTTTCTACAGGGGAGAAAAAGTGTAAAAATTTTTTAAAAATATGTTTTTCCAGGACA 3900  
Db 3841 TTAAGTTTTCTACAGGGGAGAAAAAGTGTAAAAATTTTTTAAAAATATGTTTTTCCAGGACA 3900

Qy 3901 CTTCACTTCCAAAGTCAGGTAGGTAGTCAATCTAGTTGTTAGCCCAAGGACCTCAAGGACTG 3960  
Db 3901 CTTCACTTCCAAAGTCAGGTAGGTAGTCAATCTAGTTGTTAGCCCAAGGACCTCAAGGACTG 3960  
Qy 3961 AATTTGTTTAAACATAAGGCTTTCTGTGTTGCGGAGCCGCACTTCATTAATAATCTTCTA 4020  
Db 3961 AATTTGTTTAAACATAAGGCTTTCTGTGTTGCGGAGCCGCACTTCATTAATAATCTTCTA 4020  
Qy 4021 AAACCTGTATGTTTAAAGCTTAAGCAAGACTTTTTCCTCTCTCATGAGTTGTGAAT 4080  
Db 4021 AAACCTGTATGTTTAAAGCTTAAGCAAGACTTTTTCCTCTCTCATGAGTTGTGAAT 4080  
Qy 4081 TTAATGCAACAAGCTGTAGTGGCTAACAGTTTATTTTAAAGAAATGTTTAAAGAAATGCTGT 4140  
Db 4081 TTAATGCAACAAGCTGTAGTGGCTAACAGTTTATTTTAAAGAAATGTTTAAAGAAATGCTGT 4140  
Qy 4141 TGCTTCAGGTTCTTAAATCACTCAGCACTCCAACCTTCTTAATCAAAATTTTGGAGACTTA 4200  
Db 4141 TGCTTCAGGTTCTTAAATCACTCAGCACTCCAACCTTCTTAATCAAAATTTTGGAGACTTA 4200  
Qy 4201 ACAGCATTTGCTGTGTTGAACATAAAAGCACCGGATCTTTTCCATCTAATTCGCA 4260  
Db 4201 ACAGCATTTGCTGTGTTGAACATAAAAGCACCGGATCTTTTCCATCTAATTCGCA 4260  
Qy 4261 AAAATGATCATTTGCAAAAGTCAAACTATAGCCATATCCAAATCTTTCCCTCCCA 4320  
Db 4261 AAAATGATCATTTGCAAAAGTCAAACTATAGCCATATCCAAATCTTTCCCTCCCA 4320  
Qy 4321 GAGTCTCAGTGTCTACATGTAGACTATCTTCTCTGTATAAAGTTCACCTAGGATTT 4380  
Db 4321 GAGTCTCAGTGTCTACATGTAGACTATCTTCTCTGTATAAAGTTCACCTAGGATTT 4380  
Qy 4381 CAAAGTCACCACCTATTTTACATTTTAGTCATGCAAGAAATCAAGTAGTTTGCATAAGT 4440  
Db 4381 CAAAGTCACCACCTATTTTACATTTTAGTCATGCAAGAAATCAAGTAGTTTGCATAAGT 4440  
Qy 4441 ACTTATCTTTATTTGTAATAAATTTAGTCTGTGATCAAAAGCAATTCCTAATTTTGGAG 4500  
Db 4441 ACTTATCTTTATTTGTAATAAATTTAGTCTGTGATCAAAAGCAATTCCTAATTTTGGAG 4500  
Qy 4501 AACTGGTTTTAGCATTTCAACACTAAATCCAGTTAATTAATTAATAGTTTATATGCC 4560  
Db 4501 AACTGGTTTTAGCATTTCAACACTAAATCCAGTTAATTAATTAATAGTTTATATGCC 4560  
Qy 4561 TTTCTGCTACATTTGGTTTTTCCCTGTCCCTTTGATTACGGGCTAAGGTAGGGTAAG 4620  
Db 4561 TTTCTGCTACATTTGGTTTTTCCCTGTCCCTTTGATTACGGGCTAAGGTAGGGTAAG 4620  
Qy 4621 ANNGGCTAGTGTATATAATGTGATTTGGCCCTGTGTATATGATATTTTGTAT 4680  
Db 4621 ANNGGCTAGTGTATATAATGTGATTTGGCCCTGTGTATATGATATTTTGTAT 4680  
Qy 4681 TTTTCTCTTATATATTTTACATTTTACATTTTGTGTTTCCATTTTAGGGGAT 4740  
Db 4681 TTTTCTCTTATATATTTTACATTTTACATTTTGTGTTTCCATTTTAGGGGAT 4740  
Qy 4741 AAAATTTGATTTTGAACATATGAATGGAGACTACCGCCCGCAGCATTAGTTTTCACATGATA 4800  
Db 4741 AAAATTTGATTTTGAACATATGAATGGAGACTACCGCCCGCAGCATTAGTTTTCACATGATA 4800  
Qy 4801 TACCTTTTAAACCGGAATCATTTGTTTATTTTCCCTGATTACAGGTTGTGAATGGGAAA 4860  
Db 4801 TACCTTTTAAACCGGAATCATTTGTTTATTTTCCCTGATTACAGGTTGTGAATGGGAAA 4860  
Qy 4861 GGGGCTAGTATATCAGTAGGATATACATATGGATGTATATATCATTCGTTTAGAGAA 4920  
Db 4861 GGGGCTAGTATATCAGTAGGATATACATATGGATGTATATATCATTCGTTTAGAGAA 4920  
Qy 4921 ATGAATATAAATGGGCTGGGCTCAGTGGCTCAGCGCTGTAAATCCAGCACTTTGGGAGG 4980  
Db 4921 ATGAATATAAATGGGCTGGGCTCAGTGGCTCAGCGCTGTAAATCCAGCACTTTGGGAGG 4980

Qy 4981 CTGAGGCGAGTGGATCAGCAGGTCAGGAGATCGAGACCATCTGCTTAACACGGTGAAC 5040  
Db 4981 CTGAGGCGAGTGGATCAGCAGGTCAGGAGATCGAGACCATCTGCTTAACACGGTGAAC 5040  
Qy 5041 CCCGCTCTACTATAAAAAACAGAAATTTAGCCGGCGTGGTGGCGGCGCTGTAGTCCCA 5100  
Db 5041 CCCGCTCTACTATAAAAAACAGAAATTTAGCCGGCGTGGTGGCGGCGCTGTAGTCCCA 5100  
Qy 5101 GCTACTCCGGAGGCTGAGCGAGGAGAAATGGTGTAAACCCGGGAGCGAGCTTGCAGTGA 5160  
Db 5101 GCTACTCCGGAGGCTGAGCGAGGAGAAATGGTGTAAACCCGGGAGCGAGCTTGCAGTGA 5160  
Qy 5161 GCCGAGATCTCGCCACTGCACCTCCAGCCTGGGCAACAGAGCAAGACTCTGTCTCAAAAA 5220  
Db 5161 GCCGAGATCTCGCCACTGCACCTCCAGCCTGGGCAACAGAGCAAGACTCTGTCTCAAAAA 5220  
Qy 5221 AAAAAAAG 5232  
Db 5221 AAAAAAAG 5232

RESULT 2  
AAK89468  
ID AAK89468 standard; DNA; 8763 BP.  
XX  
AC AAK89468;  
XX  
DT 05-NOV-2001 (first entry)  
XX  
DE Human digestive system antigen genomic sequence SEQ ID NO: 3044.  
XX  
KW Human; digestive system antigen; gene therapy; cancer; appendicitis;  
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;  
KW digestive system disorder; Meckel's diverticulum; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200155314-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US01324.  
XX  
PR 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.





Db 181 CAGTTAAACCTTTTGGGCGCAATGTGAATGTAATGATTTTATGTTTCTCCTGCTTGT 240  
Qy 2584 GGATGAAATAATTTCTGAGTGGTAGTTTTTTTGACAGGTAGACCATGCTCTTATCTTGTTT 2643  
Db 241 GGATGAAATAATTTCTGAGTGGTAGTTTTTTTGACAGGTAGACCATGCTCTTATCTGTTT 300  
Qy 2644 CAAATAAGTATTTCTGATTTTGTAAATGAAATATAAAATATGATGCTCAGATCTTCCAAT 2703  
Db 301 CAAATAAGTATTTCTGATTTTGTAAATGAAATATAAAATATGATGCTCAGATCTTCCAAT 360  
Qy 2704 TAAATAGTAAAGGATTCATCTTAACTCTGCTAGTCTTAAAGCTTAAAGCTGCTTAACTTTACT 2763  
Db 361 TAAATAGTAAAGGATTCATCTTAACTCTGCTAGTCTTAAAGCTTAAAGCTGCTTAACTTTACT 420  
Qy 2764 AAAAGATCTTTGTTAACTCAGTATTTTAAACATCTGTCAGCTTATGTAGGTAAAGTAGA 2823  
Db 421 AAAAGATCTTTGTTAACTCAGTATTTTAAACATCTGTCAGCTTATGTAGGTAAAGTAGA 480  
Qy 2824 AGCATGTTGTACACTGCTGTAGTATTTAGTGACAGCTTTCCATGTTGAGATTTCTCATAT 2883  
Db 481 AGCATGTTGTACACTGCTGTAGTATTTAGTGACAGCTTTCCATGTTGAGATTTCTCATAT 540  
Qy 2884 CATCTGTATCTTAAAGTTTCATGTAGTATTTTACCGTTAGGATGATTAAGATGATATA 2943  
Db 541 CATCTGTATCTTAAAGTTTCATGTAGTATTTTACCGTTAGGATGATTAAGATGATATA 600  
Qy 2944 GGACAAATGTTAAAGTCTTCTCTACCTACATTTGTTTCTCGCTAGTAAATAGTAGTA 3003  
Db 601 GGACAAATGTTAAAGTCTTCTCTACCTACATTTGTTTCTCGCTAGTAAATAGTAGTA 660  
Qy 3004 GATACCTCTGAAATAAATGTTCTCTCAAGATCTTAAACCTCTTGGAAATTTATAAAAT 3063  
Db 661 GATACCTCTGAAATAAATGTTCTCTCAAGATCTTAAACCTCTTGGAAATTTATAAAAT 720  
Qy 3064 ATTGCCAGAAAAGAGNATAGTGTGTTTAAATATTTTAAAAACACTTGAATAAGNAT 3123  
Db 721 ATTGCCAGAAAAGAGNATAGTGTGTTTAAATATTTTAAAAACACTTGAATAAGNAT 780  
Qy 3124 CAGTAGGATTAATACTAGAACGTTTAAAAATGCCCTATAGAACGTCACAGGTTTACATTTAC 3183  
Db 781 CAGTAGGATTAATACTAGAACGTTTAAAAATGCCCTATAGAACGTCACAGGTTTACATTTAC 840  
Qy 3184 AAGATTTCAACAACAAACCCATTTAGAGGTAGTAGGATGATTTACTTACAGAGGAAAGT 3243  
Db 841 AAGATTTCAACAACAAACCCATTTAGAGGTAGTAGGATGATTTACTTACAGAGGAAAGT 900  
Qy 3244 TTGAGAGTAAACGTTAAACAAATTTATTTTGTGTTGTTTCTTAAGAGAAAGAGTATTTG 3303  
Db 901 TTGAGAGTAAACGTTAAACAAATTTATTTTGTGTTGTTTCTTAAGAGAAAGAGTATTTG 960  
Qy 3304 TTATGTTCTCCTAACTCTGTTGATTTACTACTTTTAAAGTGATATTCATTTAAACATTTGCA 3363  
Db 961 TTATGTTCTCCTAACTCTGTTGATTTACTACTTTTAAAGTGATATTCATTTAAACATTTGCA 1020  
Qy 3364 AATTTATTTTATTTATTTATTTTCTTTTGTGAGATGAGTCTTCTGTCACCCAGGCTG 3423  
Db 1021 AATTTATTTTATTTATTTATTTTCTTTTGTGAGATGAGTCTTCTGTCACCCAGGCTG 1080  
Qy 3424 GAGTGCACTGAGTGATCTGCTGCTCACTGCAACCTCCGCTTCTGGGTTCAGGCAATTTCT 3483  
Db 1081 GAGTGCACTGAGTGATCTGCTGCTCACTGCAACCTCCGCTTCTGGGTTCAGGCAATTTCT 1140  
Qy 3484 CGTGCTCAGCTTCTCCTGAGTAGTGGAAATTAACAGCAGGTGCCACCATGCCCCGACTAAT 3543  
Db 1141 CGTGCTCAGCTTCTCCTGAGTAGTGGAAATTAACAGCAGGTGCCACCATGCCCCGACTAAT 1200  
Qy 3544 TTTTTTATTTTTTATGAGAGAGGGGTTTACCATGTTGGCCAGGCTGGTATCAAACTCC 3603  
Db 1201 TTTTTTATTTTTTATGAGAGAGGGGTTTACCATGTTGGCCAGGCTGGTATCAAACTCC 1260  
Qy 3604 TGACCTCAAGAGATCCACTCGCTTGGCTTCCCTCCCAAGCTGCTGGGATTTACAGGCTTGACC 3663  
|||||

Db 1261 TGACCTCAAGAGATCCACTCGCTTGGCTTCCCAAGTGGCTTACAGGCTTGAGCC 1320  
Qy 3664 ACCAGCCCGCTAAACATTTGCAATTTAAATGAGAGTTTTTAAATAATGACT 3723  
Db 1321 ACCAGCCCGCTAAACATTTGCAATTTAAATGAGAGTTTTTAAATAATGACT 1380  
Qy 3724 GCCCTGTTCTGTTTTAGTATGTAATCCTCAGTTCCTCAGCTTTGCACTGTCTGCCACT 3783  
Db 1381 GCCCTGTTCTGTTTTAGTATGTAATCCTCAGTTCCTCAGCTTTGCACTGTCTGCCACT 1440  
Qy 3784 TAGTTGCTTATATAGTACATTAACCTTGAATTTGGTCTGTATAGTCTAGACTTTAAATTTA 3843  
Db 1441 TAGTTGCTTATATAGTACATTAACCTTGAATTTGGTCTGTATAGTCTAGACTTTAAATTTA 1500  
Qy 3844 AAGTTTTCTACAAGGGGAGAAAGTGTAAAAATTTTTTAAAAATATGTTTTCCAGGACACTT 3903  
Db 1501 AAGTTTTCTACAAGGGGAGAAAGTGTAAAAATTTTTTAAAAATATGTTTTCCAGGACACTT 1560  
Qy 3904 CACTTCCAAGTCAGTAGGTAGTTCATCTAGTGTGTTAGCCCAAGACTCAAGGACTGAAT 3963  
Db 1561 CACTTCCAAGTCAGTAGGTAGTTCATCTAGTGTGTTAGCCCAAGACTCAAGGACTGAAT 1620  
Qy 3964 TGTTTTAAACATAAGGCTTTTCTGTTCTGGGAGCGGCACTTCATTTAAATTTCTTTCTAAAA 4023  
Db 1621 TGTTTTAAACATAAGGCTTTTCTGTTCTGGGAGCGGCACTTCATTTAAATTTCTTTCTAAAA 1680  
Qy 4024 CTTCTATGTTTATAGTGTAAAGCAAGACTTTTTTTTCTCTCTCCATGAGTGTGGAATTTA 4083  
Db 1681 CTTCTATGTTTATAGTGTAAAGCAAGACTTTTTTTTCTCTCTCCATGAGTGTGGAATTTA 1740  
Qy 4084 ATGCACAACGCTGATGCGGTAAACAAGTTTATTTTAAAGATTTGTTTAAAGATGCTGTTGC 4143  
Db 1741 ATGCACAACGCTGATGCGGTAAACAAGTTTATTTTAAAGATTTGTTTAAAGATGCTGTTGC 1800  
Qy 4144 TTCAGGTTCTTAAATCACTCAGCACCTCCAACTTCTTAATCAAAATTTTTTGGAGACTTAACA 4203  
Db 1801 TTCAGGTTCTTAAATCACTCAGCACCTCCAACTTCTTAATCAAAATTTTTTGGAGACTTAACA 1860  
Qy 4204 GCATTTGCTGTTGTTGAACCTATAAAAAGCACCGGATCTTTTCCATCTAAATTCGCAAAA 4263  
Db 1861 GCATTTGCTGTTGTTGAACCTATAAAAAGCACCGGATCTTTTCCATCTAAATTCGCAAAA 1920  
Qy 4264 ATTGATCAATTTGCAAGTCAAAACTATAGCCATATFCCAAATCTTTTCCCTCCCAAGAG 4323  
Db 1921 ATTGATCAATTTGCAAGTCAAAACTATAGCCATATFCCAAATCTTTTCCCTCCCAAGAG 1980  
Qy 4324 TTCTCAGTGTCTACATGTAGACTATTCCTTTCTGTATAAAGTTTCACTCTAGGATTTCAA 4383  
Db 1981 TTCTCAGTGTCTACATGTAGACTATTCCTTTCTGTATAAAGTTTCACTCTAGGATTTCAA 2040  
Qy 4384 GTCACCACTTATTTTACATTTTAGTCATGCAAAAGATTCCAAGTAGTTTTTGCATTAAGTACT 4443  
Db 2041 GTCACCACTTATTTTACATTTTAGTCATGCAAAAGATTCCAAGTAGTTTTTGCATTAAGTACT 2100  
Qy 4444 TATCTTATTTTGTAAATTAATTTAGTCTGCTGATCAAAAGCATTTGCTTAATTTTTTGAGAAC 4503  
Db 2101 TATCTTATTTTGTAAATTAATTTAGTCTGCTGATCAAAAGCATTTGCTTAATTTTTTGAGAAC 2160  
Qy 4504 TGGTTTTAGCATTTTACAAACTTAAATTTCCAGTTAAATTAATTAATAGCTTTATATGCTTTT 4563  
Db 2161 TGGTTTTAGCATTTTACAAACTTAAATTTCCAGTTAAATTAATTAATAGCTTTATATGCTTTT 2220  
Qy 4564 CCTGCTACATTTGTTTTTTTTTCCCTGTCCTTTGATTTACGGGCTAAGGTAGGTAAGANN 4623  
Db 2221 CCTGCTACATTTGTTTTTTTTTCCCTGTCCTTTTATTTACGGGCTAAGGTAGGTAAGANN 2279  
Qy 4624 GGGTGTAGTGTATATTAATGATTTGGCCCTGTGATTTATGATTTTATTTTATTTT 4683  
Db 2280 GGGTGTAGTGTATATTAATGATTTGGCCCTGTGATTTATGATTTTATTTTATTTT 2339  
Qy 4684 TGTGTTATATTTATTTACATTTTCACTTTGTTTTTGTGTTTTTGTGTTTTTGTGTTTTT 4743  
Db 2340 TGTGTTATATTTATTTACATTTTCACTTTGTTTTTGTGTTTTTGTGTTTTTGTGTTTTT 2399  
|||||

Qy 4744 ATTTGTTATTTTGAACATATGAATGAGACTACCGCCCGCAGCATTAGTTTCACATGATATAC 4803  
Db 2400 ATTTGTTATTTTGAACATATGAATGAGACTACCGCCCGCAGCATTAGTTTCACATGATATAC 2459

Qy 4804 CCTTTAAACCCGAATCATGTTGTTTATTTTCGTGATTACACAGGTGTTGAATGGGAAAGG 4863  
Db 2460 CCTTTAAACCCGAATCATGTTGTTTATTTTCCCTGATTACACAGGTGTTGAATGGGAAAGG 2519

Qy 4864 GCTAGTATATCAGTAGGATATACATGCGGATGATATATATATATATCATGCTGTTAGAAATG 4923  
Db 2520 GCTAGTATATCAGTAGGATATACATGCGGATGATATATATATATATCATGCTGTTAGAAATG 2579

Qy 4924 AAATAAAATGGGCTGGGCTCAGTGGCTCAGCGCCTGTAATCCAGCACTTTGGGAGGCTG 4983  
Db 2580 AAATAAAATGGGCTGGGCTCAGTGGCTCAGCGCCTGTAATCCAGCACTTTGGGAGGCTG 2639

Qy 4984 AGGAGGTGGATCAGAGGTGAGAGATCGAGACCATCTCTGGCTTAACACAGGTGAAACCCC 5043  
Db 2640 AGGAGGTGGATCAGAGGTGAGAGATCGAGACCATCTCTGGCTTAACACAGGTGAAACCCC 2699

Qy 5044 GTCTCTACTAAACAAACAGAAATTAGCGGCGGTGGTGGCGGCGCCTGTAGTCCCGACT 5103  
Db 2700 GTCTCTACTAAACAAACAGAAATTAGCGGCGGTGGTGGCGGCGCCTGTAGTCCCGACT 2759

Qy 5104 ACTCGGAGGCTGAGCGAGGAGATGGTGTGAACCCGGGAGGCAGAGCTTCAGCTGAGCC 5163  
Db 2760 ACTCGGAGGCTGAGCGAGGAGATGGTGTGAACCCGGGAGGCAGAGCTTCAGCTGAGCC 2819

Qy 5164 GAGATCTCGCCACTGCACTCCAGCCTGGGCAACAGAGCAAGACTCTGTCTCAAAAAAAA 5223  
Db 2820 GAGATCTCGCCACTGCACTCCAGCCTGGGCAACAGAGCAAGACTCTGTCTCAAAAAAAA 2879

Qy 5224 AAAAAA 5230  
Db 2880 AAAAAA 2886

RESULT 3  
ID ABK93875 standard; cDNA; 3000 BP.  
XX  
AC ABK93875;  
XX  
DT 26-AUG-2002 (first entry)  
XX  
DE Human cDNA encoding inhibitor of apoptosis, XIAP #2.  
XX  
KW Human; ss; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;  
KW cytosolic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;  
KW pancreatic cancer; embryonic development; viral pathogenesis;  
KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;  
KW lupus erythematosus; herpes virus infection; pox virus infection;  
KW adenovirus infection; proliferative disease.  
XX  
OS Homo sapiens.  
XX  
XX Wo200226968-A2.  
XX  
XX 04-APR-2002.  
XX  
XX 27-SEP-2001; 2001WO-CA01379.  
XX  
XX 28-SEP-2000; 2000US-0672717.  
XX  
XX (UYOT-) UNIV OTTAWA.  
XX  
XX (AEGE-) AEGERA THERAPEUTICS INC.  
XX  
XX Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;  
XX  
XX WPI; 2002-479562/51.  
XX  
XX Novel antisense inhibitor of apoptosis nucleic acid useful for

enhancing apoptosis in a cell, for treating cancer and other  
proliferative diseases -  
Example 2; Fig 15; 135pp; English.  
XX

The invention relates to an inhibitor of apoptosis (IAP) antisense  
nucleic acid (I) that inhibits IAP biological activity, regardless of  
length of the antisense nucleic acid, the IAP proteins may be mouse  
or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical  
composition comprising a mammalian IAP antisense molecule and a method of  
enhancing apoptosis in a cell, comprising administering a negative  
regulator of the IAP anti-apoptotic pathway to the cell. The IAP  
antisense inhibitor is useful for enhancing apoptosis in a cell in a  
mammal diagnosed with a proliferative disease. The method is useful for  
treating a patient diagnosed with a proliferative disease like cancer.  
The IAP antisense molecule is useful to treat, ameliorate, improve,  
sustain or prevent proliferative diseases (e.g. ovarian cancer,  
adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or  
conditions where apoptosis is involved or implicated (e.g. embryonic  
development, viral pathogenesis, autoimmune disorders, neurodegenerative  
diseases, multiple sclerosis, lupus erythematosus and infection by herpes  
virus, pox virus and adenovirus). The present sequence is a human IAP  
cDNA sequence.

Sequence 3000 BP; 974 A; 452 C; 601 G; 973 T; 0 other;  
Query Match 43.5%; Score 2278; DB 24; Length 3000;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2328; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAAGGTGGCAAGTCCCTATTTTCAAGAGAAGATGACTTTTAAACAGTTTGAAGGATCT 60  
Db 657 GAAAGGTGGCAAGTCCCTATTTTCAAGAGAAGATGACTTTTAAACAGTTTGAAGGATCT 716

Qy 61 AAAACTGTGTACCTGCAGACATCAATAAGGAAGAATTTGTAGAGAGTTTAATAGA 120  
Db 717 AAAACTGTGTACCTGCAGACATCAATAAGGAAGAATTTGTAGAGAGTTTAATAGA 776

Qy 121 TTAATAACTTTTGTCTTAATTTTCCCAAGTGTAGTCTGTTTTCAGCATCAACACTGCACGA 180  
Db 777 TTAATAACTTTTGTCTTAATTTTCCCAAGTGTAGTCTGTTTTCAGCATCAACACTGCACGA 836

Qy 181 GCAGGGTTTCTTTTACTGGTCAAGGAGATACCGTGCCTGCTTTAGTTGTCTATGCAGCT 240  
Db 837 GCAGGGTTTCTTTTACTGGTCAAGGAGATACCGTGCCTGCTTTAGTTGTCTATGCAGCT 896

Qy 241 GTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAGATFCCCAAAAT 300  
Db 897 GTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAGATFCCCAAAAT 956

Qy 301 TGCAGATTATCAACGGCTTTTATCTTCAAAATAGTCCACGCACTCTACAAATTCCTGCT 360  
Db 957 TGCAGATTATCAACGGCTTTTATCTTCAAAATAGTCCACGCACTCTACAAATTCCTGCT 1016

Qy 361 ATCCAGATGCTCAGTACAAAGTTGAAACTATCTGGAAGACAGAGATCATTTTCCTTTA 420  
Db 1017 ATCCAGATGCTCAGTACAAAGTTGAAACTATCTGGAAGACAGAGATCATTTTCCTTTA 1076

Qy 421 GACAGGCCATCTGAGACACATGCGAGACTATCTTTTGAGAACTGGGCAGGTTGTAGATATA 480  
Db 1077 GACAGGCCATCTGAGACACATGCGAGACTATCTTTTGAGAACTGGGCAGGTTGTAGATATA 1136

Qy 481 TCAGACACCATATACCCGAGGAACCTCCCATGTATCTAGAGAGCTAGATTAAGTCC 540  
Db 1137 TCAGACACCATATACCCGAGGAACCTCCCATGTATCTAGAGAGCTAGATTAAGTCC 1196

Qy 541 TTTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTCTGGACTC 600  
Db 1197 TTTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTCTGGACTC 1256

Qy 601 TACTACACAGGTATGGTGACCAAGTGCAGTCTTTTCTGTGGTGGAAAACTGAAAAAT 660  
Db 1257 TACTACACAGGTATGGTGACCAAGTGCAGTCTTTTCTGTGGTGGAAAACTGAAAAAT 1316

QY 661 TGGGAACCTTGTGATCGTGCCTGGTCAGAACACAGCGACACTTTCCTAAATGCTCTTT 720  
DB 1317 TGGGAACCTTGTGATCGTGCCTGGTCAGAACACAGCGACACTTTCCTAAATGCTCTTT 1376  
QY 721 GTTTTGGCGCGAAATCTTAATATTCGAAGTGAATCTGATGCTGAGTTCGATAGGAAT 780  
DB 1377 GTTTTGGCGCGAAATCTTAATATTCGAAGTGAATCTGATGCTGAGTTCGATAGGAAT 1436  
QY 781 TTCCCAAAATTCACAAATCTTCCAAAGAAATCCATCCATGGCAGATTAACAAGCACGGATC 840  
DB 1437 TTCCCAAAATTCACAAATCTTCCAAAGAAATCCATCCATGGCAGATTAACAAGCACGGATC 1496  
QY 841 TTTTACTTTTGGGACATGGATATACCTTACAGTAAAGAGGACAGCTTGCAGAGCTGGATTT 900  
DB 1497 TTTTACTTTTGGGACATGGATATACCTTACAGTAAAGAGGACAGCTTGCAGAGCTGGATTT 1556  
QY 901 TATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTTCACCTGPGGAGGAGGCTAACTGAT 960  
DB 1557 TATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTTCACCTGPGGAGGAGGCTAACTGAT 1616  
QY 961 TGGAGCCCGAGTGAAGCCCTTGGCAACAACATGCTAAATGGTATCCAGGGTGCAAAATAT 1020  
DB 1617 TGGAGCCCGAGTGAAGCCCTTGGCAACAACATGCTAAATGGTATCCAGGGTGCAAAATAT 1676  
QY 1021 CTGTTTAGAACAGAGGACAGAAATATATAACAATATTTCAATTAACCTCACTTCGAG 1080  
DB 1677 CTGTTTAGAACAGAGGACAGAAATATATAACAATATTTCAATTAACCTCACTTCGAG 1736  
QY 1081 GAGTGTCTGGTGAAGAACTACTGAGAAAAACACCATCACTAACTAGAGAAATGATGATACC 1140  
DB 1737 GAGTGTCTGGTGAAGAACTACTGAGAAAAACACCATCACTAACTAGAGAAATGATGATACC 1796  
QY 1141 ATCTTTCCAAATCCATGCTGTAAGAACTATACCAATGGGTTTCAGTTTCAAGGACATTT 1200  
DB 1797 ATCTTTCCAAATCCATGCTGTAAGAACTATACCAATGGGTTTCAGTTTCAAGGACATTT 1856  
QY 1201 AAGAAATTAATGGAGGAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTCAGGTT 1260  
DB 1857 AAGAAATTAATGGAGGAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTCAGGTT 1916  
QY 1261 CTGGTTGCAGATCTAGTGAAGTCTCAGAAAGACAGATATGCAAGATGAGTCAAGTCAGACT 1320  
DB 1917 CTGGTTGCAGATCTAGTGAAGTCTCAGAAAGACAGATATGCAAGATGAGTCAAGTCAGACT 1976  
QY 1321 TCATTTACAGAAAGAGATTAGTACTCAAGAGCAGCTTAAGCGCCTCAAGAGGAGAGCTT 1380  
DB 1977 TCATTTACAGAAAGAGATTAGTACTCAAGAGCAGCTTAAGCGCCTCAAGAGGAGAGCTT 2036  
QY 1381 TGCAAAATCTGTATGATAGAAATATGCTATCGTTTTTGTTCCTTGGGACATCTAGTC 1440  
DB 2037 TGCAAAATCTGTATGATAGAAATATGCTATCGTTTTTGTTCCTTGGGACATCTAGTC 2096  
QY 1441 ACTTGTAAACAATGCTGAGGACGCTGACAAAGTGTCCCATGTGTACACAGTCATTAAT 1500  
DB 2097 ACTTGTAAACAATGCTGAGGACGCTGACAAAGTGTCCCATGTGTACACAGTCATTAAT 2156  
QY 1501 TTCAAGCAAAAATTTTATGCTTTAACTTAATCTACTATAGTAGGCACTGTATGTTGTTCT 1560  
DB 2157 TTCAAGCAAAAATTTTATGCTTTAACTTAATCTACTATAGTAGGCACTGTATGTTGTTCT 2216  
QY 1561 TATTACCTGTATGATGTGATGTGAACCTGACTTTAAGTAATCAGGATTTGAATTCCTAT 1620  
DB 2217 TATTACCTGTATGATGTGATGTGAACCTGACTTTAAGTAATCAGGATTTGAATTCCTAT 2276  
QY 1621 TAGCAATTTGCTACCAAGTAGGAAAAAAATGTACATGCGAGTGTGTTTGTGGCAATATA 1680  
DB 2277 TAGCAATTTGCTACCAAGTAGGAAAAAAATGTACATGCGAGTGTGTTTGTGGCAATATA 2336  
QY 1681 ATCTTTGATATTTCTGATTTTTCAGGCTATAGCTGCTATATCCATTTTCTACTGTTA 1740  
DB 2337 ATCTTTGATATTTCTGATTTTTCAGGCTATAGCTGCTATATCCATTTTCTACTGTTA 2396

QY 1741 TTTAATGAAACCATAGACTAAGAATAAAGAACATCATACTATACTGAACAAATGTGT 1800  
DB 2397 TTTAATGAAACCATAGACTAAGAATAAAGAACATCATACTATACTGAACAAATGTGT 2456  
QY 1801 ATTCATAGTATACTGATTTAATTTCTAAGTGTAAAGTAATTAATCATCTGGATTTTAT 1860  
DB 2457 ATTCATAGTATACTGATTTAATTTCTAAGTGTAAAGTAATTAATCATCTGGATTTTAT 2516  
QY 1861 TCTTTTCAGATAGGCTTAAACAAATGGAGCTTCTGTATATAAATGTGGAGATTAGAGTTA 1920  
DB 2517 TCTTTTCAGATAGGCTTAAACAAATGGAGCTTCTGTATATAAATGTGGAGATTAGAGTTA 2576  
QY 1921 ATCTCCCAATCACATAATTTGTTTGTGAAAAAGGAATAAATGTTTCCATGCTGGTG 1980  
DB 2577 ATCTCCCAATCACATAATTTGTTTGTGAAAAAGGAATAAATGTTTCCATGCTGGTG 2636  
QY 1981 GAAAGATAGAGATTGTTTGTAGAGTTGGTGTGTTTGTGTTTGTAGGATTTCTGTCATTTCT 2040  
DB 2637 GAAAGATAGAGATTGTTTGTAGAGTTGGTGTGTTTGTGTTTGTAGGATTTCTGTCATTTCT 2696  
QY 2041 TTTAAAGTTATAAACACAGTACTTGTGCGAATTAATTTTAAAGTGATTTGCCATTTTGT 2100  
DB 2697 TTTAAAGTTATAAACACAGTACTTGTGCGAATTAATTTTAAAGTGATTTGCCATTTTGT 2756  
QY 2101 AAAGCGTATTAAATGATAGATACTATCGAGCCAAACATGTACTGACATGAAAGATGTCA 2160  
DB 2757 AAAGCGTATTAAATGATAGATACTATCGAGCCAAACATGTACTGACATGAAAGATGTCA 2816  
QY 2161 AGATATGTTTAAGTGTAAATGCAAGTGGCAAAACACTATGTATAGTCTGAGCCAGATCA 2220  
DB 2817 AGATATGTTTAAGTGTAAATGCAAGTGGCAAAACACTATGTATAGTCTGAGCCAGATCA 2876  
QY 2221 AAGTATGATGTTTAAATATCATAGAACAAAGATTTGGAAGATATACACCAAACTG 2280  
DB 2877 AAGTATGATGTTTAAATATCATAGAACAAAGATTTGGAAGATATACACCAAACTG 2936  
QY 2281 TTAATGTTGTTTCTCTTCGGGAGGGGGGATTTGGGGAGGGGGCCCCA 2329  
DB 2937 TTAATGTTGTTTCTCTTCGGGAGGGGGGATTTGGGGAGGGGGCCCCA 2985  
RESULT 4  
AAK99405 ID AAK99405 standard; DNA; 2404 BP.  
XX AC AAK99405;  
XX DT 27-JUN-2002 (first entry)  
XX DE DNA of APP related human homologue hCP35211.  
XX KW Neuroprotective; neurotropic; transgenic fly; Alzheimer's disease; Abeta;  
KW amyloid precursor protein; tissue-specific expression control; human APP;  
KW APP pathway modulator; gene therapy; gene; ds.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX FT CDS 692..1528  
XX FT /\*tag= a  
XX FT /product= "protein of human homologue hCP35211"  
XX FT /note= "No start codon"  
PN WO200226820-A2.  
PD 04-APR-2002.  
XX 01-OCT-2001; 2001WO-EP11345.  
XX 29-SEP-2000; 2000US-236893P.  
XX 14-JUN-2001; 2001US-298309P.  
XX PA (NOVS ) NOVARTIS AG.



Qy 1680 AATCTTTGAATTTCTGTGATTTTTCAGGGTATTAGCTGTATTATCAATTTTTTTTACTGTT 1739  
Db 1681 AATCTTTGAATTTCTGTGATTTTTCAGGGTATTAGCTGTATTATCAATTTTTTTTACTGTT 1740  
Qy 1740 ATTTAAATGAAACCATAGACTAAGAAATGAAGCAATCATATCAATTAACATGACACAATGTG 1799  
Db 1741 ATTTAAATGAAACCATAGACTAAGAAATGAAGCAATCATATCAATTAACATGACACAATGTG 1800  
Qy 1800 TATTCATAGTATAGTATTAATTTCTAAGTGAAGTGAATTAATCATCTGGATTTTTTA 1859  
Db 1801 TATTCATAGTATAGTATTAATTTCTAAGTGAAGTGAATTAATCATCTGGATTTTTTA 1860  
Qy 1860 TTCTTTTTCAGATAGGCTTTAAACAAATGAGCTTTCTGTATATAAATGTGGAGATAGAGTT 1919  
Db 1861 TTCTTTTTCAGATAGGCTTTAAACAAATGAGCTTTCTGTATATAAATGTGGAGATAGAGTT 1920  
Qy 1920 AATCTCCCAATCACATTAATTTGTTTGTGCAAAAAGAAATTAATTTTCCATGCTGTT 1979  
Db 1921 AATCTCCCAATCACATTAATTTGTTTGTGCAAAAAGAAATTAATTTTCCATGCTGTT 1979  
Qy 1980 GGAAGATAGAGATGTTTTTAGAGTTGTTGTTGTTTGTGTTTAGGATCTGTCCATTTTC 2039  
Db 1980 GGAAGATAGAGATGTTTTTAGAGTTGTTGTTGTTTGTGTTTAGGATCTGTCCATTTTC 2039  
Qy 2040 TTTTAAAGTTATAACACGTACTTTGTGCGAATTAATTTTTTAAAGTGAATTTGCCATTTTT 2099  
Db 2040 TTTTAAAGTTATAACACGTACTTTGTGCGAATTAATTTTTTAAAGTGAATTTGCCATTTTT 2099  
Qy 2100 GAAAGCGTATTAATGATAGATAGTACTATCGAGCCCAACATGACTGACATGGAAGATGTC 2159  
Db 2100 GAAAGCGTATTAATGATAGATAGTACTATCGAGCCCAACATGACTGACATGGAAGATGTC 2159  
Qy 2160 AAAGATATGTTAAAGTGAATGCAAGTGGCAAAACACTATGTATAGTCTGAGCCAGATC 2219  
Db 2160 AAAGATATGTTAAAGTGAATGCAAGTGGCAAAACACTATGTATAGTCTGAGCCAGATC 2219  
Qy 2220 AAAGTATGATGTTTTTAAATATGCATAGAACAAAAGATTTGGAAAGATATACACCAAACT 2279  
Db 2220 AAAGTATGATGTTTTTAAATATGCATAGAACAAAAGATTTGGAAAGATATACACCAAACT 2279  
Qy 2280 GTTAAATGTGTTCTCTTCGGGGAGGGGGGATTTGGGGG 2319  
Db 2280 GTTAAATGTGTTCTCTTCGGGGAGGGGGGATTTGGGGG 2319  
RESULT 5  
AAT70836  
ID AAT70836 standard; cDNA; 2540 BP.  
AC  
XX  
AC AAT70836;  
XX  
DT 02-SEP-1997 (first entry)  
XX  
DE Human apoptosis inhibitor xiap cDNA.  
XX  
KW Apoptosis inhibitor; x-linked inhibitor of apoptosis protein;  
KW XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome;  
KW ischaemia; myocardial infarction; stroke;  
KW reperfusion injury; toxin-induced liver disease; gene therapy;  
KW diagnosis; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key  
FT CDS 34..1527  
FT /\*tag= a  
XX  
FN WO9706255-A2.  
XX  
PD 20-FEB-1997.  
XX  
PF 05-AUG-1996; 96WO-IB01022.

XX 22-DEC-1995; 95US-0576956.  
PR 04-AUG-1995; 95US-0511485.  
XX  
PA (UYOT-) UNIV OTTAWA.  
XX  
XX Baird S, Korneluk RG, Liston P, Mackenzie AE;  
PI WPI; 1997-154262/14.  
XX P-PSDB; AAW19581.  
DR  
DR  
XX  
XX Nucleic acid encoding an inhibitor of apoptosis polypeptide - used  
PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection  
PT of susceptibility to apoptotic disease  
XX  
XX  
PS Claim 12; Page 67-68; 219pp; English.  
XX  
CC Human xiap, hiap-1 and hiap-2 genes, and murine xiap, hiap-1 and  
CC hiap-2 genes (AAT70836-41) respectively code for a new class of  
CC mammalian proteins (AAW19581-86) that are inhibitors of apoptosis  
CC (IAP). The xiap gene (for x-linked IAP gene) was isolated from a  
CC human foetal brain zapII cDNA library using an X-linked sequence  
CC tag site that shows strong homology with the conserved ring zinc  
CC finger domain of baculovirus CpiAP and OpiAP genes. The gene was  
CC assigned to chromosome Xq25 by FISH. IAP nucleic acids can be used  
CC to express IAP polypeptides in cells and animals to inhibit  
CC apoptosis, and as primers and probes to identify and isolate  
CC additional IAP genes, as well as in methods for treating diseases  
CC and disorders involving apoptosis (anti-apoptotic gene therapy).  
XX  
SQ Sequence 2540 BP; 781 A; 415 C; 570 G; 773 T; 1 other;  
Query Match 38.0%; Score 1990; DB 18; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 GAAAGGTGGACAGTCTCTATTTTCAAGAGAGATGACTTTTAAACAGTTTGAAGGATCT 60  
Db 1 GAAAGGTGGACAGTCTCTATTTTCAAGAGAGATGACTTTTAAACAGTTTGAAGGATCT 60  
Qy 61 AAAACTCTGTACCTGCAGACATCAATGAAGAGAGATTTGTAGAGAGCTTTAATAGA 120  
Db 61 AAACTCTGTACCTGCAGACATCAATGAAGAGAGATTTGTAGAGAGCTTTAATAGA 120  
Qy 121 TTAATAACTTTTGCTAATTTTCCAAAGTGTAGTCTCTGTTTTCAGCATCAACACTGTCAGCA 180  
Db 121 TTAATAACTTTTGCTAATTTTCCAAAGTGTAGTCTCTGTTTTCAGCATCAACACTGTCAGCA 180  
Qy 181 GCAGGGTTTCTTTATACCTGTTGAAGAGATACCGTGCAGTCTGCTTTAGTTGTCATGAGCT 240  
Db 181 GCAGGGTTTCTTTATACCTGTTGAAGAGATACCGTGCAGTCTGCTTTAGTTGTCATGAGCT 240  
Qy 241 GTAGATAGTGGCAATATGGAGACTTCAGCAGTTGGAAGACACAGAGAAAGTATCCCAAT 300  
Db 241 GTAGATAGTGGCAATATGGAGACTTCAGCAGTTGGAAGACACAGAGAAAGTATCCCAAT 300  
Qy 301 TGCAGATTTATCAACGGCTTTTATCTTGAAATAGTGCACGAGTCTACAAATTTCTGTT 360  
Db 301 TGCAGATTTATCAACGGCTTTTATCTTGAAATAGTGCACGAGTCTACAAATTTCTGTT 360  
Qy 361 ATCCAGAAATGTCAGTACAAAGTTGAAACATATCTGGGAAGCAGAGATCATTTTGCCTTA 420  
Db 361 ATCCAGAAATGTCAGTACAAAGTTGAAACATATCTGGGAAGCAGAGATCATTTTGCCTTA 420  
Qy 421 GACAGGCCATCTGAGACACATGCAGCTATCTTTTGAAGTGGCAGGCTGTAGATATA 480  
Db 421 GACAGGCCATCTGAGACACATGCAGCTATCTTTTGAAGTGGCAGGCTGTAGATATA 480  
Qy 481 TCAGACACCATATACCCGAGGAACCCCTGCCATGTATGTAGGAAGCTAGATTAAAGTCC 540  
Db 481 TCAGACACCATATACCCGAGGAACCCCTGCCATGTATGTAGGAAGCTAGATTAAAGTCC 540  
Qy 541 TTTCAGAACTGGCCAGAGACTATGCTCACCTAACCCCAAGAGATTAGCAAGTCTGGACTC 600

||||| 541 TTTTCAAGCTGGCCAGACTATGCTCACCTAACCCCAAGAGAGTAGCAAGTGTGACTC 600  
||||| 601 TACTACACAGGTATTTGGTGACCAAGTGCAGTGTCTTTTGGTGTGGTGAAGCAATGAAAAAT 660  
||||| 601 TACTACACAGGTATTTGGTGACCAAGTGCAGTGTCTTTTGGTGTGGTGAAGCAATGAAAAAT 660  
||||| 661 TGGGAACCTTTGTGATCGTGGCTGGTCAGAACACAGCGCACACTTCCCTAAATTTGCTTTT 720  
||||| 661 TGGGAACCTTTGTGATCGTGGCTGGTCAGAACACAGCGCACACTTCCCTAAATTTGCTTTT 720  
||||| 721 GTTTTGGCGCGGAATCTTAATATTCGAAGTGAATCTGATGCTGTGAGTTCTGATAGGAAT 780  
||||| 721 GTTTTGGCGCGGAATCTTAATATTCGAAGTGAATCTGATGCTGTGAGTTCTGATAGGAAT 780  
||||| 781 TTCCCAAAATTCACAAATCTTCCAAGAAATCCATCCATGCGCAGATTATGAAGCACGGATC 840  
||||| 781 TTCCCAAAATTCACAAATCTTCCAAGAAATCCATCCATGCGCAGATTATGAAGCACGGATC 840  
||||| 841 TTTTACTTTTGGGACATGGATATATCTCAGTTTAAACAAGGAGCAGCTTGCAGAGCTGGATTT 900  
||||| 841 TTTTACTTTTGGGACATGGATATATCTCAGTTTAAACAAGGAGCAGCTTGCAGAGCTGGATTT 900  
||||| 901 TATGCTTTTAGGTGAAGTGATAAAGTAAAGTGCTTTTCACTGTGGAGGAGGCTAACTGAT 960  
||||| 901 TATGCTTTTAGGTGAAGTGATAAAGTAAAGTGCTTTTCACTGTGGAGGAGGCTAACTGAT 960  
||||| 961 TGGAAAGCCAGTGAAGACCTTGGGACACACATGCTAAATGGTATCCAGGGTGCAATAT 1020  
||||| 961 TGGAAAGCCAGTGAAGACCTTGGGACACACATGCTAAATGGTATCCAGGGTGCAATAT 1020  
||||| 1021 CTGTTAGAACAGAGGAGCAAGAATATATAAACAATATTCATTAACTCACTTCACTTGAG 1080  
||||| 1021 CTGTTAGAACAGAGGAGCAAGAATATATAAACAATATTCATTAACTCACTTCACTTGAG 1080  
||||| 1081 GAGTGTCTGTGAAGAACTACTGAGAAACACCACATCACTAACTAGAAATTTGATGATACC 1140  
||||| 1081 GAGTGTCTGTGAAGAACTACTGAGAAACACCACATCACTAACTAGAAATTTGATGATACC 1140  
||||| 1141 ATCTTCCAAATCCTATGGTACAGAGCTATACGAATGGGTTTCAGTTTCAAGGACATT 1200  
||||| 1141 ATCTTCCAAATCCTATGGTACAGAGCTATACGAATGGGTTTCAGTTTCAAGGACATT 1200  
||||| 1201 AAGAAATAATGGAGGAAAAAATTCAGATATCTGGGAGCACTATAAATCACTTGAGGTT 1260  
||||| 1201 AAGAAATAATGGAGGAAAAAATTCAGATATCTGGGAGCACTATAAATCACTTGAGGTT 1260  
||||| 1261 CTGTTTGCAGATCTAGTGAATGCTCAGAAAGACAGTATGCAAGATGAGTCAAGTCAAGCT 1320  
||||| 1261 CTGTTTGCAGATCTAGTGAATGCTCAGAAAGACAGTATGCAAGATGAGTCAAGTCAAGCT 1320  
||||| 1321 TCATTACAGAAAGAGATTAGTACTGAGAGCAGCTAAGGCGCCTGCAAGAGGAGAAGCTT 1380  
||||| 1321 TCATTACAGAAAGAGATTAGTACTGAGAGCAGCTAAGGCGCCTGCAAGAGGAGAAGCTT 1380  
||||| 1381 TGGAAATCTGTATGGATAGAAATATTCGCTATCGTTTTTCTCTGTGACATCTAGTC 1440  
||||| 1381 TGGAAATCTGTATGGATAGAAATATTCGCTATCGTTTTTCTCTGTGACATCTAGTC 1440  
||||| 1441 ACTTGTAAACAATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGTCATTACT 1500  
||||| 1441 ACTTGTAAACAATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGTCATTACT 1500  
||||| 1501 TTCAAGCAAAAAATTTTATGCTTAACTTAACCTATAGTAGGCATGTTATGTTGTTCT 1560  
||||| 1501 TTCAAGCAAAAAATTTTATGCTTAACTTAACCTATAGTAGGCATGTTATGTTGTTCT 1560  
||||| 1561 TATTACCTGATTGAATGTGTGATGTAAGTCACTTTTAAAGTAAATCAGAGTTGAATTCAT 1620  
||||| 1561 TATTACCTGATTGAATGTGTGATGTAAGTCACTTTTAAAGTAAATCAGAGTTGAATTCAT 1620  
||||| 1621 TAGCATTTGCTACCAAGTAGGAAAAAATGTATCATGGCAGTGTGTTTGTGTCGAATATA 1680  
|||||

Db 1621 TAGCATTTGCTACCAAGTAGGAAAAAATGTATCATGGCAGTGTGTTTGTGTCGAATATA 1680  
QY 1681 ATCTTTGAAATTTCTTGATTTTTCAGGGTATTAGCTGTATTATTCATTTTACTGTTA 1740  
Db 1681 ATCTTTGAAATTTCTTGATTTTTCAGGGTATTAGCTGTATTATTCATTTTACTGTTA 1740  
QY 1741 TTTAATTTGAACCATAGACTAAGAATAAAGAGCATCATATAAATGAAACACAATGCT 1800  
Db 1741 TTTAATTTGAACCATAGACTAAGAATAAAGAGCATCATATAAATGAAACACAATGCT 1800  
QY 1801 ATTATAGTATAGTATTAAATTTCTAAGTGTAAAGTGAATTAATCATCTGGATTTTAT 1860  
Db 1801 ATTATAGTATAGTATTAAATTTCTAAGTGTAAAGTGAATTAATCATCTGGATTTTAT 1860  
QY 1861 TCTTTTTCAGATAGCTTAAACAAATGGAGCTTCTGTATATAAATGTGGAGATTAGAGTTA 1920  
Db 1861 TCTTTTTCAGATAGCTTAAACAAATGGAGCTTCTGTATATAAATGTGGAGATTAGAGTTA 1920  
QY 1921 ATCTCCCAATACATAAATTTGTTTGTGTGAAAAAGGAATAAATGTTCCATGCTGGTG 1980  
Db 1921 ATCTCCCAATACATAAATTTGTTTGTGTGAAAAAGGAATAAATGTTCCATGCTGGTG 1980  
QY 1981 GAAAGATAGAGATTGTTTTTAGAGGTTGGTGTGTTTGTGTTTAGGATTCTGTCCATTTTCT 2040  
Db 1981 GAAAGATAGAGATTGTTTTTAGAGGTTGGTGTGTTTGTGTTTAGGATTCTGTCCATTTTCT 2040  
QY 2041 T 2041  
Db 2041 T 2041  
  
RESULT 6  
AAA64901  
ID AAA64901 standard; DNA; 2540 BP.  
XX  
AC AAA64901;  
XX  
DT 07-NOV-2000 (first entry)  
XX  
DE Human X-linked inhibitor of apoptosis DNA.  
XX  
KW X-linked inhibitor of apoptosis; XIAP; hIAP; MIHA; U45880;  
KW antisense; antiinflammatory; cytostatic; tumour; ds.  
XX  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 34..1527  
FT /\*tag= a  
FT /product= "X-linked inhibitor of apoptosis"  
XX  
PN US6087173-A.  
XX  
PD 11-JUL-2000.  
XX  
PF 09-SEP-1999; 99US-0392580.  
XX  
PR 09-SEP-1999; 99US-0392580.  
XX  
PI (ISIS-) ISIS PHARM INC.  
XX  
PI Bennett CF, Cowser LM, Ackermann EJ;  
DR WPL; 2000-498201/44.  
DR P-PSDB; AAY99985.  
XX  
PT Antisense compound useful for research reagents, diagnostics,  
PT prophylaxis and for treating disorders associated with X-linked  
PT inhibitor of apoptosis, modulates expression of X-linked inhibitor of  
PT apoptosis -  
XX  
PS Example 13; Column 43-48; 33pp; English.  
XX



CC The present invention relates to antisense oligonucleotides designed to  
CC inhibit expression of the human x-linked inhibitor of apoptosis. The  
CC present sequence is the x-linked inhibitor of apoptosis DNA.  
CC Modified phosphorothioate 2'-methoxyethyl (2'-MOE) oligonucleotides are  
CC more effective inhibitors than unmodified oligonucleotides. The  
CC oligonucleotides may be used to inhibit x-linked inhibitor of apoptosis  
CC expression in cells and tissues in vitro. The oligonucleotides are also  
CC useful for treating animals or humans, prone to a disease associated  
CC with x-linked inhibitor of apoptosis. The oligonucleotides may also be  
CC used prophylactically to prevent infection, inflammation or tumour  
CC formation.  
XX

SQ Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 other;

Query Match 38.0%; Score 1990; DB 21; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAAGGTGGACAGTCTATTTTCAAGAGAGATGACTTTTAAACAGTTTGAAGGATCT 60  
Db 1 GAAAGGTGGACAGTCTATTTTCAAGAGAGATGACTTTTAAACAGTTTGAAGGATCT 60  
Qy 61 AAAACCTCTGTACCTGCAGACATCAATTAAGGAAGAAGATTTGTAGAGAGCTTTAATAGA 120  
Db 61 AAAACCTCTGTACCTGCAGACATCAATTAAGGAAGAAGATTTGTAGAGAGCTTTAATAGA 120  
Qy 121 TTAATAACTTTTGGCTTAATTTTCCAAAGTGGTAGTCTCTTTCCAGCATCAACACTGCGACGA 180  
Db 121 TTAATAACTTTTGGCTTAATTTTCCAAAGTGGTAGTCTCTTTCCAGCATCAACACTGCGACGA 180  
Qy 181 GCAGGGTTCTTTATACGTGGTGAAGAGATACCGTGCCTGCTTTAGTGTGATGACAGCT 240  
Db 181 GCAGGGTTCTTTATACGTGGTGAAGAGATACCGTGCCTGCTTTAGTGTGATGACAGCT 240  
Qy 241 GTAGATAGTGCATATGGAGATCGACAGTGTGAAGACACAGAGAGTATCCCAAT 300  
Db 241 GTAGATAGTGCATATGGAGATCGACAGTGTGAAGACACAGAGAGTATCCCAAT 300  
Qy 301 TGCAGATTTATCAAGGGCTTTTATCTTGAATAATAGTGCAGCGAGTCTACAAATCTCGT 360  
Db 301 TGCAGATTTATCAAGGGCTTTTATCTTGAATAATAGTGCAGCGAGTCTACAAATCTCGT 360  
Qy 361 ATCCAGATGTGACATCAAAAGTTGAAACATATCTGGGAAGCAGAGATCATTTGGCCCTTA 420  
Db 361 ATCCAGATGTGACATCAAAAGTTGAAACATATCTGGGAAGCAGAGATCATTTGGCCCTTA 420  
Qy 421 GACAGCCATCTGACACACATGACAGTATCTTTTGAGAACTGGGCGAGTTGTAGATATA 480  
Db 421 GACAGCCATCTGACACACATGACAGTATCTTTTGAGAACTGGGCGAGTTGTAGATATA 480  
Qy 481 TCAGACACATATACCCGAGGAACCTGCCATGTATAGTGAAGAGCTAGATTTAAAGTCC 540  
Db 481 TCAGACACATATACCCGAGGAACCTGCCATGTATAGTGAAGAGCTAGATTTAAAGTCC 540  
Qy 541 TTTGAGAACTGGCCAGACTATGCTCACTCACTCAACCCCAAGAGAGTTAGCAAGTCTGGACTC 600  
Db 541 TTTGAGAACTGGCCAGACTATGCTCACTCACTCAACCCCAAGAGAGTTAGCAAGTCTGGACTC 600  
Qy 601 TACTACACAGTATTTGGTACCAAGTGCAGTCTTTTGTGTTGGTGGAAACTGAAAT 660  
Db 601 TACTACACAGTATTTGGTACCAAGTGCAGTCTTTTGTGTTGGTGGAAACTGAAAT 660  
Qy 661 TGGGAACCTTGTGTCGTCGCTGCTCAGAACACAGGCGACACTTTCCCTAAATGCTTCCTTT 720  
Db 661 TGGGAACCTTGTGTCGTCGCTGCTCAGAACACAGGCGACACTTTCCCTAAATGCTTCCTTT 720  
Qy 721 GTTTTGGCCCGGAATCTTAAATATTCGAAGTGAATCTGTGCTGCTGATGAGGAAT 780  
Db 721 GTTTTGGCCCGGAATCTTAAATATTCGAAGTGAATCTGTGCTGCTGATGAGGAAT 780  
Qy 781 TTCCCAATTTCAACAAATCTTCCAGAAATCCATCCATGGCAGATATGAGACGCGATC 840  
Db 781 TTCCCAATTTCAACAAATCTTCCAGAAATCCATCCATGGCAGATATGAGACGCGATC 840

Qy 841 TTTACTTTTGGACATGGATATACTCAGTTAACRAGGACAGCTTGCAGAGCTGGATTT 900  
Db 841 TTTACTTTTGGACATGGATATACTCAGTTAACRAGGACAGCTTGCAGAGCTGGATTT 900  
Qy 901 TATGCTTTAGGTGAAGGTGATAAAGTGCCTTTTCACTGTGGAGGAGGCTTAAGTAT 960  
Db 901 TATGCTTTAGGTGAAGGTGATAAAGTGCCTTTTCACTGTGGAGGAGGCTTAAGTAT 960  
Qy 961 TGGAGCCCTGAGACCTTTGGGAACAACATGCTAATGGTATCCAGGCTGCAAAAT 1020  
Db 961 TGGAGCCCTGAGACCTTTGGGAACAACATGCTAATGGTATCCAGGCTGCAAAAT 1020  
Qy 1021 CTGTTAGAACAGAGGACAAAGATATATAACAATATTTCAATTTAACTCACTTACG 1080  
Db 1021 CTGTTAGAACAGAGGACAAAGATATATAACAATATTTCAATTTAACTCACTTACG 1080  
Qy 1081 GAGTGTCTGTTAAGACTTACTGAGAAAACACCATCACTTAAGTAAGTAATGATGATACC 1140  
Db 1081 GAGTGTCTGTTAAGACTTACTGAGAAAACACCATCACTTAAGTAAGTAATGATGATACC 1140  
Qy 1141 ATCTTCCAAAATCCTATGCTACAAAGACTATACGAATGGGTTTCAGTTTCAAGGACAT 1200  
Db 1141 ATCTTCCAAAATCCTATGCTACAAAGACTATACGAATGGGTTTCAGTTTCAAGGACAT 1200  
Qy 1201 AAGAAAATAATGGAGGAAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTTGAGGTT 1260  
Db 1201 AAGAAAATAATGGAGGAAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTTGAGGTT 1260  
Qy 1261 CTGTTGCAGATCTAGTGAATGCTCAGAAAACAGTATGCAAGTATGATGATGATGAT 1320  
Db 1261 CTGTTGCAGATCTAGTGAATGCTCAGAAAACAGTATGCAAGTATGATGATGATGAT 1320  
Qy 1321 TCATTACAGAAAGAGATTAGTACTGAAGAGCAGCTAAGCGCCTGCAAGAGAGAGGCTT 1380  
Db 1321 TCATTACAGAAAGAGATTAGTACTGAAGAGCAGCTAAGCGCCTGCAAGAGAGAGGCTT 1380  
Qy 1381 TGCAAAATCTGTATGGATAGAAATATTTCTATCTGTTTTTGTTCCTTTGTTGGACATCTAGTC 1440  
Db 1381 TGCAAAATCTGTATGGATAGAAATATTTCTATCTGTTTTTGTTCCTTTGTTGGACATCTAGTC 1440  
Qy 1441 ACTTGTAAACAAATGTGCTGAAGAGCTTGCAGAAAGTGTCCCATGTGCACAGTCAAT 1500  
Db 1441 ACTTGTAAACAAATGTGCTGAAGAGCTTGCAGAAAGTGTCCCATGTGCACAGTCAAT 1500  
Qy 1501 TTTCAAGCAAAAATTTTATCTCTTAATCTAATCTAGTAGGAGCTTATGTTGTTCT 1560  
Db 1501 TTTCAAGCAAAAATTTTATCTCTTAATCTAATCTAGTAGGAGCTTATGTTGTTCT 1560  
Qy 1561 TATTACCTGATTTGAATGTGTGATGTGAACCTGAACTTTAAGTAATCAGGATTTGAATTCAT 1620  
Db 1561 TATTACCTGATTTGAATGTGTGATGTGAACCTGAACTTTAAGTAATCAGGATTTGAATTCAT 1620  
Qy 1621 TAGCATTTGCTACCAAGTGAAGAAAAAATGTACATGCGAGTGTGTTAGTTGGCAATATA 1680  
Db 1621 TAGCATTTGCTACCAAGTGAAGAAAAAATGTACATGCGAGTGTGTTAGTTGGCAATATA 1680  
Qy 1681 ATCTTTGAATTTCTGATTTTTCAGGGTATTTAGCTGTATTTATCCATTTTCTTACTGTTA 1740  
Db 1681 ATCTTTGAATTTCTGATTTTTCAGGGTATTTAGCTGTATTTATCCATTTTCTTACTGTTA 1740  
Qy 1741 TTTAATTTGAAACCATAGACTAAGAAATAAGAGCATCATCTATAACTGAACACAAATGTT 1800  
Db 1741 TTTAATTTGAAACCATAGACTAAGAAATAAGAGCATCATCTATAACTGAACACAAATGTT 1800  
Qy 1801 ATTCATAGTATACGATTTAATTTCTAAGTGAAGTGAATTAATCACTGATGATTTTAT 1860  
Db 1801 ATTCATAGTATACGATTTAATTTCTAAGTGAAGTGAATTAATCACTGATGATTTTAT 1860  
Qy 1861 TCTTTTCAGATAGGCTTAACAAATGGAGCTTCTGCTATATAAATCTGAGATTAGAGTTA 1920  
Db 1861 TCTTTTCAGATAGGCTTAACAAATGGAGCTTCTGCTATATAAATCTGAGATTAGAGTTA 1920

QY 1921 ATCTCCCAATCACATAAATTTGTTTGTGAAAAAGAAATAAATTTGTTCCATGCTGGTG 1980  
Db 1921 ATCTCCCAATCACATAAATTTGTTTGTGAAAAAGAAATAAATTTGTTCCATGCTGGTG 1980  
QY 1981 GAAAGATAGAGATGTTTGTAGAGTTGGTTGTTGTTTGTAGATTTCTGTCATTTTCT 2040  
Db 1981 GAAAGATAGAGATGTTTGTAGAGTTGGTTGTTGTTTGTAGATTTCTGTCATTTTCT 2040  
QY 2041 T 2041  
Db 2041 T 2041  
RESULT 7  
ABK93869  
ID ABK93869 standard; cDNA; 2540 BP.  
XX  
AC ABK93869;  
XX  
DT 26-AUG-2002 (first entry)  
XX  
DE Human cDNA encoding inhibitor of apoptosis, XIAP #1.  
XX  
KW Human; ss: gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;  
KW cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;  
KW pancreatic cancer; embryonic development; viral pathogenesis;  
KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;  
KW lupus erythematosus; herpes virus infection; pox virus infection;  
KW adenovirus infection; proliferative disease.  
XX  
OS Homo sapiens.  
XX  
XX W0200226968-A2.  
XX  
XX 04-APR-2002.  
XX  
XX 27-SEP-2001; 2001W0-CA01379.  
XX  
XX 28-SEP-2000; 2000US-067217.  
XX  
XX (UYOR-) UNIV OTTAWA.  
XX (AEGE-) AEGERA THERAPEUTICS INC.  
XX  
XX Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;  
XX  
XX WPI; 2002-479562/51.  
XX P-PSDB; ABG65663.  
XX  
XX Novel antisense inhibitor of apoptosis nucleic acid useful for  
XX enhancing apoptosis in a cell, for treating cancer and other  
XX proliferative diseases -  
XX  
XX Disclosure; Fig 1; 135pp; English.  
XX  
XX The invention relates to an inhibitor of apoptosis (IAP) antisense  
XX nucleic acid (I) that inhibits IAP biological activity, regardless of  
XX length of the antisense nucleic acid, the IAP proteins may be mouse  
XX or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical  
XX composition comprising a mammalian IAP antisense molecule and a method of  
XX enhancing apoptosis in a cell, comprising administering a negative  
XX regulator of the IAP anti-apoptotic pathway to the cell. The IAP  
XX antisense inhibitor is useful for enhancing apoptosis in a cell in a  
XX mammal diagnosed with a proliferative disease. The method is useful for  
XX treating a patient diagnosed with a proliferative disease like cancer.  
XX The IAP antisense molecule is useful to treat, ameliorate, improve,  
XX sustain or prevent proliferative diseases (e.g. ovarian cancer,  
XX adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or  
XX conditions where apoptosis is involved or implicated (e.g. embryonic  
XX development, viral pathogenesis, autoimmune disorders, neurodegenerative  
XX diseases, multiple sclerosis, lupus erythematosus and infection by herpes  
XX virus, pox virus and adenovirus). The present sequence is a human IAP  
XX cDNA sequence.

SQ Sequence 2540 BP; 782 A; 415 C; 549 G; 772 T; 22 other;  
Query Match 37.6%; Score 1969; DB 24; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2019; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 22 TTTCAGAGAGAGATGACCTTTTAAACAGTTTGAAGGATCTAAACCTTGTTACCTGCAGAC 81  
Db 22 TTTCAGAGAGAGATGACCTTTTAAACAGTTTGAAGGATCTAAACCTTGTTACCTGCAGAC 81  
QY 82 ATCAATAAGGAAGAATAATTTGTAGAAGAGTTTAATAGATATAAAACCTTTTGCTAAATTTT 141  
Db 82 ATCAATAAGGAAGAATAATTTGTAGAAGAGTTTAATAGATATAAAACCTTTTGCTAAATTTT 141  
QY 142 CCAAGTGGTAGTCCTGTTTTCAGCATCAACACTGGCAGCAGCAGGTTTCTTTATACGGT 201  
Db 142 CCAAGTGGTAGTCCTGTTTTCAGCATCAACACTGGCAGCAGCAGGTTTCTTTATACGGT 201  
QY 202 GAAGGAGATACCGTGGTGGTCTTTAGTTGTCATGCAGCTGTAGATAGATGGCAATATGGA 261  
Db 202 GAAGGAGATACCGTGGTGGTCTTTAGTTGTCATGCAGCTGTAGATAGATGGCAATATGGA 261  
QY 262 GACTCAGCAGTTGGAAGACACAGAGAAAGTATCCCAATTTGCAGATTTATCAACGGCTTT 321  
Db 262 GACTCAGCAGTTGGAAGACACAGAGAAAGTATCCCAATTTGCAGATTTATCAACGGCTTT 321  
QY 322 TATCTTCAAAATAGTGCAGCAGCTCTACAAATTTCTGGTATCCAGAAATGGTCAGTACAAA 381  
Db 322 TATCTTCAAAATAGTGCAGCAGCTCTACAAATTTCTGGTATCCAGAAATGGTCAGTACAAA 381  
QY 382 GTTGAAATATCTCTGGGAAGCAGAGATCATTTTGCCTTTAGACAGCCATCTGAGACACAT 441  
Db 382 GTTGAAATATCTCTGGGAAGCAGAGATCATTTTGCCTTTAGACAGCCATCTGAGACACAT 441  
QY 442 GCAGACTATCTTTTGAGAACTGGGCGAGTTGTAGATATATCAGACACATATACCCGAGG 501  
Db 442 GCAGACTATCTTTTGAGAACTGGGCGAGTTGTAGATATATCAGACACATATACCCGAGG 501  
QY 502 AACCTTCCCATGTATAGTGAAGCTAGATTAAGTCTTTCAGAACTGGCCAGACTAT 561  
Db 502 AACCTTCCCATGTATGTGAAGAAGCTAGATTAAGTCTTTCAGAACTGGCCAGACTAT 561  
QY 562 GCTCACCTAACCCCAAGAGAGTTAGCAAGTGTCTGAGCTCTACTACAGAGTTATTTGGTGAC 621  
Db 562 GCTCACCTAACCCCAAGAGAGTTAGCAAGTGTCTGAGCTCTACTACAGAGTTATTTGGTGAC 621  
QY 622 CAAGTGCAGTGTCTTTTGTGGTGGAAACTGAAAAATTTGGGAACCTTTGTGATCGTGCC 681  
Db 622 CAAGTGCAGTGTCTTTTGTGGTGGAAACTGAAAAATTTGGGAACCTTTGTGATCGTGCC 681  
QY 682 TGGTCAACAACACAGGCGACACTTTCCCTAATTTGCTTCTTTTGGGCGGGAATCTTAAT 741  
Db 682 TGGTCAACAACACAGGCGACACTTTCCCTAATTTGCTTCTTTTGGGCGGGAATCTTAAT 741  
QY 742 ATTCGAAGTGAATCTGATGCTGTGAGTTCGTATAGGAATTTCCCAAAATTTCAACAAATCTT 801  
Db 742 ATTCGAAGTGAATCTGATGCTGTGAGTTCGTATAGGAATTTCCCAAAATTTCAACAAATCTT 801  
QY 802 CCAAGAAATCCATCCATGGCAGATTTAAGACACGGATCTTTACTTTTGGGACATGGATA 861  
Db 802 CCAAGAAATCCATCCATGGCAGATTTAAGACACGGATCTTTACTTTTGGGACATGGATA 861  
QY 862 TACTCAGTTTAACAGGAGCAGCTTGCAGAGCTGGATTTTATGCTTTAGGTGAAGGTGAT 921  
Db 862 TACTCAGTTTAACAGGAGCAGCTTGCAGAGCTGGATTTTATGCTTTAGGTGAAGGTGAT 921  
QY 922 AAGTAAAGTGTCTTCACTGTGGAGGAGGCTAACTGATTTGAAGCCAGTGAAGACCTT 981  
Db 922 AAGTAAAGTGTCTTCACTGTGGAGGAGGCTAACTGATTTGAAGCCAGTGAAGACCTT 981  
QY 982 TGGGAACAACATGCTAAATGGTATCCAGGGTGCAAAATATCTGTTTAGAACAGAGGACAA 1041  
Db 982 TGGGAACAACATGCTAAATGGTATCCAGGGTGCAAAATATCTGTTTAGAACAGAGGACAA 1041

```
Qy 1042 GAAATATATAACAATATTCATTCTTAACCTCATTCACCTGTGAGGAGTGTCTGGTAAGAACAATCTACT 1101
Db 1042 GAAATATATAACAATATTCATTCTTAACCTCATTCACCTGTGAGGAGTGTCTGGTAAGAACAATCTACT 1101
Qy 1102 GAGAAACACCATCATCTACTACTAGAGAAATTCATGATACCATCTTCCAAAATCCCTATGGTA 1161
Db 1102 GAGAAACACCATCATCTACTACTAGAGAAATTCATGATACCATCTTCCAAAATCCCTATGGTA 1161
Qy 1162 CAAGAAGCTATACGAATGGGTTTCAGTTTCAAGGACATTAAGAAATTAATGGAGGAAAA 1221
Db 1162 CAAGAAGCTATACGAATGGGTTTCAGTTTCAAGGACATTAAGAAATTAATGGAGGAAAA 1221
Qy 1222 ATTCAGATATCTGGGAGCAACTATAAATCACTTGAGGTTCTGGTTGCGAGATCTAGTGAAT 1281
Db 1222 ATTCAGATATCTGGGAGCAACTATAAATCACTTGAGGTTCTGGTTGCGAGATCTAGTGAAT 1281
Qy 1282 GCTCAGAAGACAGTATCGAAGAGAGTCAAGTCAGATCTTCAATACAGAAAGAGATTAAGT 1341
Db 1282 GCTCAGAAGACAGTATCGAAGAGAGTCAAGTCAGATCTTCAATACAGAAAGAGATTAAGT 1341
Qy 1342 ACTGAAGACAGCTAAGCGGCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGA 1401
Db 1342 ACTGAAGACAGCTAAGCGGCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGA 1401
Qy 1402 AATATGCTATCGTTTGTTCCTTGTGGACATCTAGTCACTTGTAAACAATGTCGTGAA 1461
Db 1402 AATATGCTATCGTTTGTTCCTTGTGGACATCTAGTCACTTGTAAACAATGTCGTGAA 1461
Qy 1462 GCAGTTGACAGTGTCCCATGTGTACACAGTCATTAATCTTCAAGCAAAAATTTTATG 1521
Db 1462 GCAGTTGACAGTGTCCCATGTGTACACAGTCATTAATCTTCAAGCAAAAATTTTATG 1521
Qy 1522 TCTTAATCTAATCTATAGTAGGAGTATGTTGTTCTTATATCCCTGATTAATGATGAT 1581
Db 1522 TCTTAATCTAATCTATAGTAGGAGTATGTTGTTCTTATATCCCTGATTAATGATGAT 1581
Qy 1582 GATGTGAACCTGACTTTAAGTAATCAGGATTAATCCATTAAGCAATTTGCTACCAAGTAGG 1641
Db 1582 GATGTGAACCTGACTTTAAGTAATCAGGATTAATCCATTAAGCAATTTGCTACCAAGTAGG 1641
Qy 1642 AAAAAAATGACATGGCAGTGTGTTAGTTGGCAATATAATCTTTGAATTTCTTGATTTT 1701
Db 1642 AAAAAAATGACATGGCAGTGTGTTAGTTGGCAATATAATCTTTGAATTTCTTGATTTT 1701
Qy 1702 TCAGGTTATAGCTGTATATCCATTTTCTTCTGTTTATTAATGAAACCATAGACTA 1761
Db 1702 TCAGGTTATAGCTGTATATCCATTTTCTTCTGTTTATTAATGAAACCATAGACTA 1761
Qy 1762 AGAATAAGAAGCATCATACTATACTGAACACAATGCTATTCATAGTATAGTATTAAT 1821
Db 1762 AGAATAAGAAGCATCATACTATACTGAACACAATGCTATTCATAGTATAGTATTAAT 1821
Qy 1822 TTTCTAAGTGTAAAGTAATTAATCATCTGGATTTTATTTCTTTTCAGATAGGCTTAACA 1881
Db 1822 TTTCTAAGTGTAAAGTAATTAATCATCTGGATTTTATTTCTTTTCAGATAGGCTTAACA 1881
Qy 1882 AATGAGCTTTCTGTATATAATGTTGGAGATTAGAGTTAATCTCCCAATCACATAATTT 1941
Db 1882 AATGAGCTTTCTGTATATAATGTTGGAGATTAGAGTTAATCTCCCAATCACATAATTT 1941
Qy 1942 GTTTTGTGAAAAAGGAATAAATGTTTCCATGCTGGTGGAAAGATAGAGATTTGTTTTTA 2001
Db 1942 GTTTTGTGAAAAAGGAATAAATGTTTCCATGCTGGTGGAAAGATAGAGATTTGTTTTTA 2001
Qy 2002 GAGGTTGTTGTTGTTTGGATTTCTGTCATTTCTT 2041
Db 2002 GAGGTTGTTGTTGTTTGGATTTCTGTCATTTCTT 2041
```

RESULT 8  
AAZ48862  
ID, AAZ48862 standard; cDNA; 1659 BP.

```
XX AAZ48862;  
XX AC  
XX XX  
DT 24-MAR-2000 (first entry)  
XX  
DE Human XIAP coding sequence.  
XX  
KW Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta;  
KW transforming growth factor-beta activated kinase 1; monocytic migration;  
KW TAK1 binding protein 1; extracellular matrix protein production;  
KW cell growth inhibitor; beta-amyloid protein deposition;  
KW immunosuppression; Transforming growth factor-beta; ds.  
XX  
OS Homo sapiens.  
XX OS  
XX JPI1326328-A.  
XX PN  
XX  
PD 26-NOV-1999.  
XX  
PF 13-MAY-1998; 98JP-0130378.  
XX PF  
XX 13-MAY-1998; 98JP-0130378.  
XX PR  
XX (MATSU) MATSUMOTO K.  
XX PA  
XX WPI; 2000-078337/07.  
XX DR  
XX P-PSDB; AAY59451.  
XX  
PT Screening a substance which inhibits combination of the X-linked  
PT inhibitor of apoptosis protein -  
XX  
XX Disclosure; Page 28-30; 43pp; Japanese.  
XX  
CC This sequence encodes the human XIAP protein.  
CC The invention relates to a method for screening a substance inhibiting  
CC the formation of a complex between XIAP and TAB1, in which X-linked  
CC inhibitor of apoptosis protein (XIAP), transforming growth factor-beta  
CC activated kinase 1(TAK1) binding protein 1(TAB1) and a substance to be  
CC tested are contacted with each other and then the presence or formation  
CC of a complex between XIAP and TAB1 is detected. The substance can be used  
CC as a drug for extracellular matrix protein production enhancement, cell  
CC growth inhibition, monocytic migration, physiologically active substance  
CC induction, immunosuppression, and beta-amyloid protein deposition. A  
CC substance inhibiting the formation of a complex between TAB1 and XIAP as  
CC well as between XIAP and TGF-beta (transforming growth factor-beta) type  
CC I and/or type II receptor is useful as a drug.  
XX  
XX Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 other;  
SQ  
Query Match 29.8%; Score 1560; DB 21; Length 1659;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1610; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 GAAAGGTGGACAGTCTCTATTTTCAAGAGAGATGACTTTTACAGTTTGAAGGATCT 60  
Db 49 GAAAGGTGGACAGTCTCTATTTTCAAGAGAGATGACTTTTACAGTTTGAAGGATCT 108  
Qy 61 AAAACTTGTGTACCTGCGACATCAATAAGGAAGAAGATTTGTAGAAGAGCTTTAATAGA 120  
Db 109 AAAACTTGTGTACCTGCGACATCAATAAGGAAGAAGATTTGTAGAAGAGCTTTAATAGA 168  
Qy 121 TTAATAACTTTTGTCTAATTTTCCAAAGTGGTAGTCTCTGTTTCAGCATCAACACTGGCAGCA 180  
Db 169 TTAATAACTTTTGTCTAATTTTCCAAAGTGGTAGTCTCTGTTTCAGCATCAACACTGGCAGCA 228  
Qy 181 GCAGGTTTCTTTTACTGTGGTGAAGGAGATACCGTGGCGGTGCTTTAGTGTGTCAGCT 240  
Db 229 GCAGGTTTCTTTTACTGTGGTGAAGGAGATACCGTGGCGGTGCTTTAGTGTGTCAGCT 288  
Qy 241 GTAGATAGTGGCAATATGGAGACTCAGCAGTTGGAAGACACAGAGAAAGTATCCCAAT 300  
Db 289 GTAGATAGTGGCAATATGGAGACTCAGCAGTTGGAAGACACAGAGAAAGTATCCCAAT 348
```

```
QY 301 TGCAGATTTATCAACGGCTTTTATCTGTGAAATAGTGCCACGAGTCTACAAATTCCTGGT 360
DB 349 TGCAGATTTATCAACGGCTTTTATCTGTGAAATAGTGCCACGAGTCTACAAATTCCTGGT 408
QY 361 ATCCAGAAATGGTCAGTACAAAGTTGAAACTATCTCGGGAAGCAGACATCATTTTGGCTT 420
DB 409 ATCCAGAAATGGTCAGTACAAAGTTGAAACTATCTCGGGAAGCAGACATCATTTTGGCTT 468
QY 421 GACAGGCCATCTCAGACACATGACAGACTATCTTTTGTAGAACTGGCAGGTTGTAGATATA 480
DB 469 GACAGGCCATCTCAGACACATGACAGACTATCTTTTGTAGAACTGGCAGGTTGTAGATATA 528
QY 481 TCAGACACCATATACCCGAGGAACCCCTGCCATGTATAGTGAAGAAGCTAGATATAAGTCC 540
DB 529 TCAGACACCATATACCCGAGGAACCCCTGCCATGTATAGTGAAGAAGCTAGATATAAGTCC 588
QY 541 TTTTCAGAACTGGCCAGACATATGCTACCTAACCCCAAGAGAGTTAGCAAGTGTGACATC 600
DB 589 TTTTCAGAACTGGCCAGACATATGCTACCTAACCCCAAGAGAGTTAGCAAGTGTGACATC 648
QY 601 TACTACACAGGTATTGGTGTACCAAGTGCAGTGTCTTTTGTGTGGTGGAAAACTGAAAAAT 660
DB 649 TACTACACAGGTATTGGTGTACCAAGTGCAGTGTCTTTTGTGTGGTGGAAAACTGAAAAAT 708
QY 661 TGGGAACCTTGTGATCGTGCCTGGTCAGAACACAGCGACACTTCCCTAATTCCTTCTTT 720
DB 709 TGGGAACCTTGTGATCGTGCCTGGTCAGAACACAGCGACACTTCCCTAATTCCTTCTTT 768
QY 721 GTTTTGGCCGGAATCTTAATATTCGAAGTGAATCTGATGCTGTGAGTCTGATAGAAT 780
DB 769 GTTTTGGCCGGAATCTTAATATTCGAAGTGAATCTGATGCTGTGAGTCTGATAGAAT 828
QY 781 TTCCCAAAATCAAAATCTTCCAAAGAAATCCATCATGCGCAGATATGAAGCACGGATC 840
DB 829 TTCCCAAAATCAAAATCTTCCAAAGAAATCCATCATGCGCAGATATGAAGCACGGATC 888
QY 841 TTTTACTTTTGGGACATGGATATATCTCAGTTTAAACAAGSAGCAGCTTCAAGAGCTGGATTT 900
DB 889 TTTTACTTTTGGGACATGGATATATCTCAGTTTAAACAAGSAGCAGCTTCAAGAGCTGGATTT 948
QY 901 TATGCTTTTAGTGAAGTGAATAAGTAAAGTGTCTTTCACGTGTGGAGGAGGCTAACTGAT 960
DB 949 TATGCTTTTAGTGAAGTGAATAAGTAAAGTGTCTTTCACGTGTGGAGGAGGCTAACTGAT 1008
QY 961 TGAAGCCAGTCAAGACCTTGGGAACACATCTGCTAAATGGTATCCAGGTCGCAATAT 1020
DB 1009 TGAAGCCAGTCAAGACCTTGGGAACACATCTGCTAAATGGTATCCAGGTCGCAATAT 1068
QY 1021 CTGTTAGAACAAGGAGCAAGAATATATAACAATATTCATTAACTCAATTCACCTTGAG 1080
DB 1069 CTGTTAGAACAAGGAGCAAGAATATATAACAATATTCATTAACTCAATTCACCTTGAG 1128
QY 1081 GAGTGTCTGTAGAACTACTGAGAAACACCATCACTAACTAGAAGATTTGATGATACC 1140
DB 1129 GAGTGTCTGTAGAACTACTGAGAAACACCATCACTAACTAGAAGATTTGATGATACC 1188
QY 1141 ATCTTCAAAATCTATGGTACAAAGAGCTATACGAATGGGTTTCAGTTTCAAGGACATTT 1200
DB 1189 ATCTTCAAAATCTATGGTACAAAGAGCTATACGAATGGGTTTCAGTTTCAAGGACATTT 1248
QY 1201 AAGAAATATGAGGAGGAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTGAGGTT 1260
DB 1249 AAGAAATATGAGGAGGAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTGAGGTT 1308
QY 1261 CTGGTTGCAGATCTAGTGAATGCTCAGAAAGACAGATATGCAAGATGAGTCAAGTCAAGCT 1320
DB 1309 CTGGTTGCAGATCTAGTGAATGCTCAGAAAGACAGATATGCAAGATGAGTCAAGTCAAGCT 1368
QY 1321 TCATTACAGAAACAGATTAGTACTGAGAGCAGCTAAGCGCCCTGCAAGAGGAGAGCTTT 1380
DB 1369 TCATTACAGAAACAGATTAGTACTGAGAGCAGCTAAGCGCCCTGCAAGAGGAGAGCTTT 1428
QY 1381 TGCAAAATCTGTATGGATAGAAATATTCGCTATCGTTTTTCTTCTTCTGTCGACATCTAGTC 1440
```

```
DB 1429 TCGAAAATCTGTATGGATAGAAAATATTCCTATCGTTTTTCTTCTTCTGTCGACATCTAGTC 1488
QY 1441 ACTTGTAAACAATGCTGTGAAGCAGTTGACAAGTGTCCCATGTGCTTACACAGTCATTAAT 1500
DB 1489 ACTTGTAAACAATGCTGTGAAGCAGTTGACAAGTGTCCCATGTGCTTACACAGTCATTAAT 1548
QY 1501 TTCAAGCAAAAAATTTTATGTCTTAATCTTAATCTTAATCTTAATCTTAATCTTAATCTTAATCT 1560
DB 1549 TTCAAGCAAAAAATTTTATGTCTTAATCTTAATCTTAATCTTAATCTTAATCTTAATCTTAATCT 1608
QY 1561 TATTACCTGATTGAATGTGTGATGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1611
DB 1609 TATTACCTGATTGAATGTGTGATGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1659

RESULT 9
AAK89469
ID AAK89469 standard; DNA; 469 BP.
XX
AC AAK89469;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human digestive system antigen genomic sequence SEQ ID NO: 3045.
KW Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
KW digestive system disorder; Meckel's diverticulum; ds.
XX
OS Homo sapiens.
PN WO200155314-A2.
PD 02-AUG-2001.
PF
XX 17-JAN-2001; 2001WO-US01324.
XX
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
```

```
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 01-NOV-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-502630/55.
DR
XX
XX Polynucleotides encoding digestive system antigens, useful for
PT diagnosing, treating, preventing and/or prognosing disorders of the
PT digestive system, particularly cancer and cancer metastases.
XX
XX Disclosure; SEQ ID NO 3045; 986pp; English.
PS
XX
XX The present invention provides the protein and coding sequences of a
CC number of human digestive system antigens. These can be used in the
CC diagnosis, treatment and prevention of digestive system disorders,
CC including cancer, Meckel's diverticulum, bacterial or parasitic
CC infections, appendicitis, Hirschsprung's disease, chronic colitis or
CC ulcerative colitis. The present sequence is a genomic DNA fragment
CC encoding a digestive system antigen of the invention.
XX
SQ Sequence 469 BP; 150 A; 58 C; 82 G; 179 T; 0 other;
Query Match 9.0%; Score 469; DB 22; Length 469;
Best Local Similarity 100.0%; Pred. No. 1.4e-162;
Matches 469; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1522 TCCTTAATCTAAGTATAGTGGCAGTGTATGTTGTTCTTATTACCTGATTGAATGTGT 1581
Db 1 TCCTTAATCTAAGTATAGTGGCAGTGTATGTTGTTCTTATTACCTGATTGAATGTGT 60
Qy 1582 GATGTGAAGTACATTAAGTAAATCAGGATTGAATCCATTAGCATTGCTACCAAGTAGG 1641
Db 61 GATGTGAAGTACATTAAGTAAATCAGGATTGAATCCATTAGCATTGCTACCAAGTAGG 120
Qy 1642 AAAAAAATGTACATGGCAGTGTGTTTGTAGTGGCAATATAATCTTGAATTTCTTGATTTT 1701
Db 121 AAAAAAATGTACATGGCAGTGTGTTTGTAGTGGCAATATAATCTTGAATTTCTTGATTTT 180
Qy 1702 TCAGGGTATTAGCTGTATTATCCATTTTTTTTACTGTTTATTAAATGAACCATAGACTA 1761
Db 181 TCAGGGTATTAGCTGTATTATCCATTTTTTTTACTGTTTATTAAATGAACCATAGACTA 240
Qy 1762 AGAATAAGACCATCATACTATTAAGTGAACATGCTATTATCATAGTATGATTTAA 1821
Db 17-NOV-2000; 2000US-0249210.
```

Db 241 AGAATAAGAGCATCTACTATATACTGAACACAAATGTGTAATCATAGTATACATGATTAA 300  
QY 1822 TTCTTAAGTGAAGTGAATTAATCATCTGATTTTATCTTTTTCAGATAGGCTTAACA 1881  
Db 301 TTCTTAAGTGAAGTGAATTAATCATCTGATTTTATCTTTTTCAGATAGGCTTAACA 360  
QY 1882 AATGGAGCTTCTGTATATAAATGTGAGATTAGAGTTAATCTCCCAATCATATAATTT 1941  
Db 361 AATGGAGCTTCTGTATATAAATGTGAGATTAGAGTTAATCTCCCAATCATATAATTT 420  
QY 1942 GTTTTGTGTGAAAGGAATAAATCTTCCATCTGCTGGTGAAGATAGA 1990  
Db 421 GTTTTGTGTGAAAGGAATAAATCTTCCATCTGCTGGTGAAGATAGA 469

RESULT 10  
ABA43584/C  
ID ABA43584 standard; DNA; 489 BP.  
XX  
AC ABA43584;  
XX  
DT 01-FEB-2002 (first entry)  
XX  
DE Human breast cell single exon nucleic acid probe #2279.  
XX  
KW Human; microarray; single exon probe; gene expression; breast;  
KW disease; cancer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200157271-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US00662.  
XX  
PR 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-496933/54.

XX  
PT New spatially-addressable set of single exon nucleic acid probes,  
PT useful for measuring gene expression in sample derived from human  
PT breast, comprises number of single exon nucleic acid probes -  
XX  
XX  
PS Claim 1; SEQ ID NO 2279; 327pp + sequence listing; English.  
XX  
CC The invention relates to a spatially-addressable set of single exon  
CC nucleic acid probes for measuring gene expression in a sample derived  
CC from human breast and BT 474 cells. The method involves contacting  
CC the probes with a collection of detectably labelled nucleic acids  
CC derived from mRNA of human breast, and then measuring the label  
CC bound to each probe of the microarray. The probes are useful for  
CC verifying the expression of regions of genomic DNA predicted to  
CC encode proteins. They are useful for gene discovery, and for  
CC determining predisposition and/or prognosing breast disease. Gene  
CC expression analysis is useful for assessing the toxicity of chemical  
CC agents on cells. The microarray of this invention presents a far greater  
CC diversity of probes for measuring gene expression, with far less bias  
CC than expressed sequence tag microarrays. The method is suitable for  
CC rapid production of functional information from genomic sequence. The  
CC present sequence is a single exon nucleic acid probe of the invention.  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly

CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 489 BP; 175 A; 90 C; 73 G; 151 T; 0 other;  
Query Match 8.9%; Score 466; DB 22; Length 489;  
Best Local Similarity 100.0%; Pred. No. 1.7e-161;  
Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1332 AGAGATTAGTACTGAAGAGCAGCTAAGGCCCTGCAAGAGGAGAAGCTTTGCAAAATCTG 1391  
Db 466 AGAGATTAGTACTGAAGAGCAGCTAAGGCCCTGCAAGAGGAGAAGCTTTGCAAAATCTG 407  
QY 1392 TATGGATAGAAATATTGCTATCGTTTTTGTTCCTTGTGGACATCTAGTCACTTGTAAACA 1451  
Db 406 TATGGATAGAAATATTGCTATCGTTTTTGTTCCTTGTGGACATCTAGTCACTTGTAAACA 347  
QY 1452 ATGTGCTGAAGCAGTTGACAAAGTGTCCCATGTGCTACACAGTCATTACTTTTCAGCAAAA 1511  
Db 346 ATGTGCTGAAGCAGTTGACAAAGTGTCCCATGTGCTACACAGTCATTACTTTTCAGCAAAA 287  
QY 1512 AATTTTATGTCCTTAATCTAATCTATAGTAGGCATGTTATGTGTTCTTTATTTACCCCTGA 1571  
Db 286 AATTTTATGTCCTTAATCTAATCTATAGTAGGCATGTTATGTGTTCTTTATTTACCCCTGA 227  
QY 1572 TTGAATGTGTGATGTGAACCTGACTTTTAAATCAATCAGGATTGAATTCATTAGCAATTTGCT 1631  
Db 226 TTGAATGTGTGATGTGAACCTGACTTTTAAATCAATCAGGATTGAATTCATTAGCAATTTGCT 167  
QY 1632 ACCAAGTAGGAAAAAATGTAATGTACATGCGCAGTGTTTAGTTGGCAATATATAATCTTTGAATT 1691  
Db 166 ACCAAGTAGGAAAAAATGTAATGTACATGCGCAGTGTTTAGTTGGCAATATATAATCTTTGAATT 107  
QY 1692 TCTTGATTTTTCAGGGTATTAGTGTATTATCCATTTTTTTTACTGTTATTTAATTGAAA 1751  
Db 106 TCTTGATTTTTCAGGGTATTAGTGTATTATCCATTTTTTTTACTGTTATTTAATTGAAA 47  
QY 1752 CCATAGACTAAGAATAAGAAGCATCATCTACTATATACTGAACACAATG 1797  
Db 46 CCATAGACTAAGAATAAGAAGCATCATCTACTATATACTGAACACAATG 1  
RESULT 11  
AII12335/C  
ID AII12335 standard; DNA; 489 BP.  
XX  
AC AII12335;  
XX  
DT 12-OCT-2001 (first entry)  
XX  
DE Probe #2268 for gene expression analysis in human cervical cell sample.  
XX  
KW Probe; human; microarray; gene expression; cervical epithelial cell;  
KW cervical cancer; ss.  
XX  
XX  
OS Homo sapiens.  
XX  
PN WO200157278-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US00670.  
XX  
PR 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;





```
QY 1752 CCATAGACTAAGATAAGAGCATCATACATATATACTGAACACATG 1797
|||||
Db 46 CCATAGACTAAGATAAGAGCATCATACATATATACTGAACACATG 1
|||||

RESULT 13
AAH33140
ID AAH33140 standard; cDNA; 417 BP.
XX AC AAH33140;
XX DT 03-SEP-2001 (first entry)
XX DE Human colon cancer antigen encoding cDNA SEQ ID NO:196.
XX KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
XX KW colorectal carcinoma; chromosome X; ss.
XX OS Homo sapiens.
XX PN WO200122920-A2.
XX PD 05-APR-2001.
XX PF 28-SEP-2000; 2000WO-US26524.
XX PR 29-SEP-1999; 99US-0157137.
XX PR 03-NOV-1999; 99US-0163280.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX WPI: 2001-235357/24.
XX P-PSDB; AAG73709.
XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX useful for preventing, diagnosing and/or treating colorectal cancers -
XX Claim 1; Page 2344; 9803pp; English.
XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
XX cancer-associated nucleic acid molecules (N) and proteins (P), where
XX the proteins are collectively known as colon cancer antigens. The colon
XX cancer antigens have cytostatic activity and can be used in gene
XX therapy and vaccine production. N and P may be used in the prevention,
XX diagnosis and treatment of diseases associated with inappropriate P
XX expression. For example, N and P may be used to treat disorders
XX associated with decreased expression by rectifying mutations or deletions
XX in a patient's genome that affect the activity of P by expressing
XX inactive proteins or to supplement the patients own production of P.
XX Additionally, N may be used to produce the colon cancer-associated Ps,
XX by inserting the nucleic acids into a host cell and culturing the cell
XX to express the proteins. N and P can be used in the prevention, diagnosis
XX and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
XX and AAB77789 represent sequences used in the exemplification of the
XX present invention.
XX N.B. Pages 666 to 682 and page 7053 of the sequence listing were
XX missing at time of publication, meaning no sequences are present for
XX SEQ ID NO:1027 to 1052, 7921 and 7922.
XX SQ Sequence 417 BP; 118 A; 61 C; 65 G; 172 T; 1 other;

Query Match 6.9%; Score 359; DB 22; Length 417;
Best Local Similarity 99.8%; Pred. No. 3.3e-122;
Matches 409; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2350 TTTCACATTTCTACATTTTTCATTTTGTCTCTCGCAATTTTATAAGTATGATTACTT 2409
|||||
Db 1 TTTCACATTTCTACATTTTTCATTTTGTCTCTCGCAATTTTATAAGTATGATTACTT 60
|||||

QY 2410 TTGTAATCAGAATTTTGAAGAATTTTGTGCTGATTTTAAAGGCTTAGGCATGTTCAAACG 2469
|||||
```

```
Db 61 TTGTAATCAGAATTTTGAAGAATTTTGTGCTGATTTTAAAGGCTTAGGCATGTTCAAACG 120
QY 2470 CCTGCAAACTACTTATCAGTCAGCTTTAGTTTCTTAATCCAAAGAGCGGCGAGTTA 2529
|||||
Db 121 CCTGCAAACTACTTATCAGTCAGCTTTAGTTTCTTAATCCAAAGAGCGGCGAGTTA 180
|||||
QY 2530 ACCTTTGTGGTCCCAATGTGAAATGTAATGATTTTATGTTTTCCTGCTTTGTGGATGA 2589
|||||
Db 181 ACCTTTGTGGTCCCAATGTGAAATGTAATGATTTTATGTTTTCCTGCTTTGTGGATGA 240
|||||
QY 2590 AAAATATTTCTGAGTGGTAGTTTTTGCACAGGTAGACCATGCTTAATCTGTTCAAAAT 2649
|||||
Db 241 AAAATATTTCTGAGTGGTAGTTTTTGCACAGGTAGACCATGCTTAATCTGTTCAAAAT 300
|||||
QY 2650 AAGTATTTCTGATTTTGTAAATGAAATATATAAATATGTCAGATCTTCCAAATTAATTA 2709
|||||
Db 301 AAGTATTTCTGATTTTGTAAATGAAATATATAAATATGTCAGATCTTCCAAATTAATTA 360
|||||
QY 2710 GTAAGGATTCATCCTTAATCCTTGCTAGTTTAAAGCCTGCGCTAAGTCACTT 2759
|||||
Db 361 GTAAGGATTCATCCTTAATCCTTGCTAGTTTAAAGCCTGCGCTAAGTCACTT 410
|||||

RESULT 14
AAC25231
ID AAC25231 standard; cDNA; 315 BP.
XX AC AAC25231;
XX DT 06-OCT-2000 (first entry)
XX DE Human secreted protein 5' EST, SEQ ID NO: 29306.
XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX KW gene therapy; chromosome mapping; ss.
XX OS Homo sapiens.
XX PN EP1033401-A2.
XX PD 06-SEP-2000.
XX PF 21-FEB-2000; 2000EP-0200610.
XX PR 26-FEB-1999; 99US-0122487.
XX PA (GEST ) GENSET.
XX Dumas Milne Edwards J, Duclert A, Giordano J;
XX WPI: 2000-500381/45.
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
XX diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX Claim 1; SEQ ID 29306; 71pp + CD-ROM; English.
XX The present sequence is one of a large number of 5' ESTs derived from
XX mRNAs encoding secreted proteins. No ORF has yet been conclusively
XX identified within the present sequence. The 5' ESTs were prepared from
XX total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
XX sequences usually correspond mainly to the 3' untranslated region (UTR)
XX of the mRNA because they are often obtained from oligo-dT primed cDNA
XX libraries. Such ESTs are not well suited for isolating cDNA sequences
XX derived from the 5' ends of mRNAs and even in those cases where longer
XX cDNA sequences have been obtained, the full 5' UTR is rarely included.
XX 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
XX used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
XX in diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX They are used to obtain upstream regulatory sequences and to design
XX expression and secretion vectors.
XX
```



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 9, 2002, 19:48:40 ; Search time 156 Seconds  
(without alignments)  
10285.467 Million cell updates/sec

Title: US-09-974-592-3  
Perfect score: 5232  
Sequence: 1 gaaaggtgacagtccta.....tcaaaaaaaaaaaaaaaag 5232

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 15338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued\_Patents\_NA.\*  
1: /cgn2.6/ptodata/2/ina/5A\_COMB.seq.\*  
2: /cgn2.6/ptodata/2/ina/5B\_COMB.seq.\*  
3: /cgn2.6/ptodata/2/ina/6A\_COMB.seq.\*  
4: /cgn2.6/ptodata/2/ina/6B\_COMB.seq.\*  
5: /cgn2.6/ptodata/2/ina/PCTUS\_COMB.seq.\*  
6: /cgn2.6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5232	100.0	5232	US-09-212-971-3	Sequence 3, Appli
2	5232	100.0	5232	US-08-800-929A-3	Sequence 3, Appli
3	5232	100.0	5232	US-09-617-053A-3	Sequence 3, Appli
4	1990	38.0	2540	US-08-511-485-3	Sequence 3, Appli
5	1990	38.0	2540	US-09-392-580-1	Sequence 1, Appli
6	1588	30.4	1588	US-09-239-867-3	Sequence 3, Appli
7	103	2.0	40328	US-08-742-185-102	Sequence 102, App
8	103	2.0	43795	US-08-742-185-101	Sequence 101, App
9	83	1.6	152331	US-09-128-155-16	Sequence 16, Appl
10	81	1.5	3494	US-09-334-601-5	Sequence 5, Appli
11	74	1.4	19736	US-09-740-035-3	Sequence 3, Appli
12	70	1.3	11298	US-07-869-933-31	Sequence 31, Appli
13	70	1.3	11298	US-08-201-879A-2	Sequence 2, Appli
14	70	1.3	11298	US-09-103-663-31	Sequence 31, Appl
15	69	1.3	14581	US-08-520-373D-4	Sequence 4, Appli
16	69	1.3	22481	US-08-367-841A-43	Sequence 43, Appl
17	69	1.3	22481	PCT-US95-07201-43	Sequence 43, Appl
18	69	1.3	22484	US-09-875-223-2	Sequence 2, Appli
19	69	1.3	16998	US-09-676-610B-24	Sequence 24, Appl
20	67	1.3	859	US-09-535-008-58	Sequence 58, Appl
21	67	1.3	36651	US-09-738-894A-3	Sequence 3, Appli
22	67	1.3	70000	US-09-851-896-3	Sequence 3, Appli
23	66	1.3	534	US-08-599-252-101	Sequence 101, App
24	66	1.3	534	PCT-US96-06352-101	Sequence 101, App
25	66	1.3	534	PCT-US96-06583-101	Sequence 101, App
26	66	1.3	956	US-09-641-638-41	Sequence 41, Appl
27	66	1.3	1712	US-09-058-389A-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-09-212-971-3  
; Sequence 3, Application US/09212971B  
; Patent No. 6107041  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G  
; APPLICANT: Mackenzie, Alexander E  
; APPLICANT: Liston, Peter  
; APPLICANT: Baird, Stephen  
; APPLICANT: Tsang, Benjamin K  
; APPLICANT: Pratt, Christine  
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
; FILE REFERENCE: 07891/009002  
; CURRENT APPLICATION NUMBER: US/09/212,971B  
; CURRENT FILING DATE: 1998-12-16  
; EARLIER APPLICATION NUMBER: 60/017,354  
; EARLIER FILING DATE: 1996-04-26  
; EARLIER APPLICATION NUMBER: 60/030,590  
; EARLIER FILING DATE: 1996-11-14  
; EARLIER APPLICATION NUMBER: 08/800,929  
; EARLIER FILING DATE: 1997-02-13  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 5232  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: variation  
; LOCATION: (4623)...(4623)  
; OTHER INFORMATION: n can be any nucleotide  
; FEATURE:  
; NAME/KEY: variation  
; LOCATION: (4622)...(4622)  
; OTHER INFORMATION: n can be any nucleotide  
US-09-212-971-3

Query Match 100.0%; Score 5232; DB 3; Length 5232;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAAGGTGGACAAGTCCTATTTTCAAGAGAAGATGACTTTTAAACAGTTTTCGAAGGATCT 60

|||||

Db 1 GAAAGGTGGACAAGTCCTATTTTCAAGAGAAGATGACTTTTAAACAGTTTTCGAAGGATCT 60

|||||

Qy 61 AAAACTTGTGTACCTGCGAGACATCAATAAGGAAGAAGATTTGTAGAGAGTTTAATAGA 120

|||||

Db 61 AAAACTTGTGTACCTGCGAGACATCAATAAGGAAGAAGATTTGTAGAGAGTTTAATAGA 120

|||||

Qy 121 TTAATAAATCTTTGCTAAATTTTCCAAAGTGGTAGTCCTGTTTCAGCATCAACACTGGCACGA 180  
Db 121 TTAATAAATCTTTGCTAAATTTTCCAAAGTGGTAGTCCTGTTTCAGCATCAACACTGGCACGA 180  
Qy 181 GCAGGTTTCTTTATACGTGGTGAAGGAGATACCGTGCCTGCTTTAGTTGATGACGCT 240  
Db 181 GCAGGTTTCTTTATACGTGGTGAAGGAGATACCGTGCCTGCTTTAGTTGATGACGCT 240  
Qy 241 GTAGATAGTGGCAATATGGAGACTCAGCAGTGGGAACACAGAGAAAGTATCCCAAT 300  
Db 241 GTAGATAGTGGCAATATGGAGACTCAGCAGTGGGAACACAGAGAAAGTATCCCAAT 300  
Qy 301 TGCAGATTTATCAAGGCTTTTATCTTGAATAATAGTGCAGCGACTCPACAAAATCTCGT 360  
Db 301 TGCAGATTTATCAAGGCTTTTATCTTGAATAATAGTGCAGCGACTCPACAAAATCTCGT 360  
Qy 361 ATCCAGAAATGTCAGTACAAAATGTTGAAAATATCTGTTGAGAACTGGCAGGTTGTAGATATA 420  
Db 361 ATCCAGAAATGTCAGTACAAAATGTTGAAAATATCTGTTGAGAACTGGCAGGTTGTAGATATA 420  
Qy 421 GACAGGCCATCTGAGACACATGCAGACTATCTTTTGAGAACTGGCAGGTTGTAGATATA 480  
Db 421 GACAGGCCATCTGAGACACATGCAGACTATCTTTTGAGAACTGGCAGGTTGTAGATATA 480  
Qy 481 TCAGACACCATATACCCGAGGAACCTGCCATGTATAGTGAAGAGCTPAGATTTAAAGTCC 540  
Db 481 TCAGACACCATATACCCGAGGAACCTGCCATGTATAGTGAAGAGCTPAGATTTAAAGTCC 540  
Qy 541 TTTCCAGAACTGGCCAGACTATGTCACCTAACCCAGAGAGATTAGCAAGTCTGGAGTC 600  
Db 541 TTTCCAGAACTGGCCAGACTATGTCACCTAACCCAGAGAGATTAGCAAGTCTGGAGTC 600  
Qy 601 TACTACACAGTATTGGTGACCAAGTGCAGTCTTTTCTGTTGGTGGAAAACCTGAAAAT 660  
Db 601 TACTACACAGTATTGGTGACCAAGTGCAGTCTTTTCTGTTGGTGGAAAACCTGAAAAT 660  
Qy 661 TGGGAACCTTGTGATCGTCCGTGTCAGAACACAGCGCACACTTTCCCTAAATGCTTCCT 720  
Db 661 TGGGAACCTTGTGATCGTCCGTGTCAGAACACAGCGCACACTTTCCCTAAATGCTTCCT 720  
Qy 721 GTTTTGGCCCGAATCTTAATATTGGAAGTGAATCTGATGCTGAGTTCTGATAGGAAT 780  
Db 721 GTTTTGGCCCGAATCTTAATATTGGAAGTGAATCTGATGCTGAGTTCTGATAGGAAT 780  
Qy 781 TTTCCCAATTTCAACAAATCTTCCAAAGAAATCCATCCATGGCAGATTATGAAGCAGGATC 840  
Db 781 TTTCCCAATTTCAACAAATCTTCCAAAGAAATCCATCCATGGCAGATTATGAAGCAGGATC 840  
Qy 841 TTTACTTTTGGGACATGGATATCTCAGTTAACAGGAGCAGCTTGCAGAGCTGGATTT 900  
Db 841 TTTACTTTTGGGACATGGATATCTCAGTTAACAGGAGCAGCTTGCAGAGCTGGATTT 900  
Qy 901 TATGCTTTAGTGAAGTGATTAAGTAAAGTCTTCACTGTGGAGGAGGCTTAACGAT 960  
Db 901 TATGCTTTAGTGAAGTGATTAAGTAAAGTCTTCACTGTGGAGGAGGCTTAACGAT 960  
Qy 961 TGGAGCCAGTGAAGACCTTTGGGAACACATGCTAAATGTTATCCAGGTTGCAAAATAT 1020  
Db 961 TGGAGCCAGTGAAGACCTTTGGGAACACATGCTAAATGTTATCCAGGTTGCAAAATAT 1020  
Qy 1021 CTGTTTAGAACAGAGGGAAGAATATATAAACAAATATTCATTTAACTCATCTTACCTGAG 1080  
Db 1021 CTGTTTAGAACAGAGGGAAGAATATATAAACAAATATTCATTTAACTCATCTTACCTGAG 1080  
Qy 1081 GAGTGTCTGGTAAAGACTACTGAGAAACACCCATCACTAACTAGAGAAATTTGATGATACC 1140  
Db 1081 GAGTGTCTGGTAAAGACTACTGAGAAACACCCATCACTAACTAGAGAAATTTGATGATACC 1140  
Qy 1141 ATCTTCCAAAATCTTATGTTACAGAAAGCTATACGAATGGGTTTCAGTTTCAAGGACATTT 1200  
Db 1141 ATCTTCCAAAATCTTATGTTACAGAAAGCTATACGAATGGGTTTCAGTTTCAAGGACATTT 1200

Qy 1201 AAGAAAATAATGGAGGAAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTCAGGTT 1260  
Db 1201 AAGAAAATAATGGAGGAAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTCAGGTT 1260  
Qy 1261 CTGGTTGCAGATCTAGTGAATGCTCAGAAAACACAGTATGCAAGATGAGTCAAGTCAAGCT 1320  
Db 1261 CTGGTTGCAGATCTAGTGAATGCTCAGAAAACACAGTATGCAAGATGAGTCAAGTCAAGCT 1320  
Qy 1321 TCATTACAGAAAGAGATTAGTACTGAAGAGCAGCTTAAGCGCCTGCAAGAGGAGAAGCTT 1380  
Db 1321 TCATTACAGAAAGAGATTAGTACTGAAGAGCAGCTTAAGCGCCTGCAAGAGGAGAAGCTT 1380  
Qy 1381 TGCAAAATCTGTATGGATAGAAAATATGCTATCGTTTTTGTTCCTTGGACATCTAGTC 1440  
Db 1381 TGCAAAATCTGTATGGATAGAAAATATGCTATCGTTTTTGTTCCTTGGACATCTAGTC 1440  
Qy 1441 ACTTGTAAACAATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGTCAATTACT 1500  
Db 1441 ACTTGTAAACAATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGTCAATTACT 1500  
Qy 1501 TTTCAAGCAAAAAATTTTATGTTCTTAATCTAACTCTATAGTAGGCATGTTATGTTGTCT 1560  
Db 1501 TTTCAAGCAAAAAATTTTATGTTCTTAATCTAACTCTATAGTAGGCATGTTATGTTGTCT 1560  
Qy 1561 TATTACCCTGATTTGAATGTGATGTAAGTGAACCTGACCTTAAGTAAATCAGGATTGAATCCAT 1620  
Db 1561 TATTACCCTGATTTGAATGTGATGTAAGTGAACCTGACCTTAAGTAAATCAGGATTGAATCCAT 1620  
Qy 1621 TAGCAATTTGCTACCAAGTAGGAAAAAATGTACATGSCAGTGTATAGTTGGCAATATA 1680  
Db 1621 TAGCAATTTGCTACCAAGTAGGAAAAAATGTACATGSCAGTGTATAGTTGGCAATATA 1680  
Qy 1681 ATCTTTGAATTTCTGATTTTTCAGGCTATTAGCTGTATATCCCATTTTTTTTACTGTTA 1740  
Db 1681 ATCTTTGAATTTCTGATTTTTCAGGCTATTAGCTGTATATCCCATTTTTTTTACTGTTA 1740  
Qy 1741 TTTAATTTGAAACCCATPAGACTAAGAAATAAGAGCATCATATACTGAACACAATGTGT 1800  
Db 1741 TTTAATTTGAAACCCATPAGACTAAGAAATAAGAGCATCATATACTGAACACAATGTGT 1800  
Qy 1801 ATTCATAGTATCTGATTTTAATTTCTAAGTGAAGTGAATTAATCATCTGGATTTTTAT 1860  
Db 1801 ATTCATAGTATCTGATTTTAATTTCTAAGTGAAGTGAATTAATCATCTGGATTTTTAT 1860  
Qy 1861 TCTTTTCAGATAGGCTTAACAAAATGGAGCTTCTCTATATAAATGGAGATTAGAGTTA -1920  
Db 1861 TCTTTTCAGATAGGCTTAACAAAATGGAGCTTCTCTCTATATAAATGGAGATTAGAGTTA 1920  
Qy 1921 ATCTCCCCAATCACATAATTTGTTGTGTAAGAAAGAAATTAATGTTCCATGCTGGTG 1980  
Db 1921 ATCTCCCCAATCACATAATTTGTTGTGTAAGAAAGAAATTAATGTTCCATGCTGGTG 1980  
Qy 1981 GAAAGATAGAGATTGTTTTAGAGGTTGGTGTGTTTAAAGTGATTTGCAATTTTCT 2040  
Db 1981 GAAAGATAGAGATTGTTTTAGAGGTTGGTGTGTTTAAAGTGATTTGCAATTTTCT 2040  
Qy 2041 TTTAAAGTTATTAACACACCTACTTGTGCGAATTAATTTTTTAAAGTGATTTGCAATTTTG 2100  
Db 2041 TTTAAAGTTATTAACACACCTACTTGTGCGAATTAATTTTTTAAAGTGATTTGCAATTTTG 2100  
Qy 2101 AAAGCGTATTTAATGATAGAATFATCGAGCCAACTGCTACTGATGAGAAAGATGCA 2160  
Db 2101 AAAGCGTATTTAATGATAGAATFATCGAGCCAACTGCTACTGATGAGAAAGATGCA 2160  
Qy 2161 AAGATATCTTAAGTCTAAATCCAGTGGCAAAACACTATGTTATAGTCTGAGCCAGATCA 2220  
Db 2161 AAGATATCTTAAGTCTAAATCCAGTGGCAAAACACTATGTTATAGTCTGAGCCAGATCA 2220  
Qy 2221 AAGTATGTTATGTTTAAATATGATAGCAACAAAGATTGGAAAGATATACACCAACTG 2280  
Db 2221 AAGTATGTTATGTTTAAATATGATAGCAACAAAGATTGGAAAGATATACACCAACTG 2280  
Qy 2281 TTAATGTTGTTTCTCTTCGGGGAGGGGGGATTCGGGGAGGGGGCCCGAGAGGGTTTFA 2340

|||||  
Db 2281 TTAATGTGGTTCTCTCGGGAGGGGGATTTGGGGAGGGCCCGAGAGGGGTTTA 2340  
QY TAGGGCCTTTCTACTTCTACTTTTCTACTTTGTTCTGTGCTGCAATTTTATTAAGTAT 2400  
Db 2341 TAGGGCCTTTCTACTTCTACTTTTCTACTTTGTTCTGTGCTGCAATTTTATTAAGTAT 2400  
QY GTATTACTTTTGTAAATCAGAAATTTTGAAGAATTTTGTCTGATTTAAAGCTTTAGGCAT 2460  
Db 2401 GTATTACTTTTGTAAATCAGAAATTTTGAAGAATTTTGTCTGATTTAAAGCTTTAGGCAT 2460  
QY GTTCAAACGCCGTGCAAACTACTTATCACCTCAGCTTTAGTTTTTCTTAATCCAAAGGCA 2520  
Db 2461 GTTCAAACGCCGTGCAAACTACTTATCACCTCAGCTTTAGTTTTTCTTAATCCAAAGGCA 2520  
QY GGGCAGTTAACTTTTGGTGCCAAATGTGAATCTAAATGATTTATGTTTTTCTCGCTT 2580  
Db 2521 GGGCAGTTAACTTTTGGTGCCAAATGTGAATCTAAATGATTTATGTTTTTCTCGCTT 2580  
QY TGTGGATGAAAAATATTCTGAGTGGTAGTTTTTGTGACAGGTAGACCATGTCTTATCTTG 2640  
Db 2581 TGTGGATGAAAAATATTCTGAGTGGTAGTTTTTGTGACAGGTAGACCATGTCTTATCTTG 2640  
QY TTTCAAATAAGTATTTCTGATTTTGTAAATGAAATATAAATAATATGCTCAGATCTTCC 2700  
Db 2641 TTTCAAATAAGTATTTCTGATTTTGTAAATGAAATATAAATAATATGCTCAGATCTTCC 2700  
QY AATTAATAGTAAGGATTCATCCCTTAATCCTTGCTAGTTTAAAGCCTGCCTAAGTCACATT 2760  
Db 2701 AATTAATAGTAAGGATTCATCCCTTAATCCTTGCTAGTTTAAAGCCTGCCTAAGTCACATT 2760  
QY ACTAAAAGATCTTTGTTAACTCAGTATTTTAAACATCTGTCAGCTTATGTAGTAAAAAGT 2820  
Db 2761 ACTAAAAGATCTTTGTTAACTCAGTATTTTAAACATCTGTCAGCTTATGTAGTAAAAAGT 2820  
QY AGAAGCATGTTTGTACACTGCTTGTAGTTATAGTGACAGCTTTCCATGTTGAGATCTCA 2880  
Db 2821 AGAAGCATGTTTGTACACTGCTTGTAGTTATAGTGACAGCTTTCCATGTTGAGATCTCA 2880  
QY TATCATCTTGATCTTAAAGTTTCATGTGAGTTTTTTACCGTTAGATGATTAAGATGAT 2940  
Db 2881 TATCATCTTGATCTTAAAGTTTCATGTGAGTTTTTTACCGTTAGATGATTAAGATGAT 2940  
QY ATAGGCAAAAATGTTAAAGTCTTCTCTACCTACATTTGTTTTCTGGCTAGTAAATAGTA 3000  
Db 2941 ATAGGCAAAAATGTTAAAGTCTTCTCTACCTACATTTGTTTTCTGGCTAGTAAATAGTA 3000  
QY GTAGATCTTCTGAATAAATGTTCTCTCAAGATCTTAAACCTCTTGGAAATATAAA 3060  
Db 3001 GTAGATCTTCTGAATAAATGTTCTCTCAAGATCTTAAACCTCTTGGAAATATAAA 3060  
QY AATATTGGCAAGAAAGAAATAGTTGTTTAAATATTTTTTAAAAACACTTGAATAAG 3120  
Db 3061 AATATTGGCAAGAAAGAAATAGTTGTTTAAATATTTTTTAAAAACACTTGAATAAG 3120  
QY AATCAGTAGGGTATAAATCTAGAAAGTTAAAAATGCCTCATAGAAGCTCCAGGGTTTACAT 3180  
Db 3121 AATCAGTAGGGTATAAATCTAGAAAGTTAAAAATGCCTCATAGAAGCTCCAGGGTTTACAT 3180  
QY TACAAGATTTCTACAACAAACCCATTTGAGAGGTGAGTAAGGCATGTTTACTACAGAGAA 3240  
Db 3181 TACAAGATTTCTACAACAAACCCATTTGAGAGGTGAGTAAGGCATGTTTACTACAGAGAA 3240  
QY AGTTTGGAGTAAACACTGTAATAAATATATTTTTTGTGTTACTTCTAAGAGAAAGAGTA 3300  
Db 3241 AGTTTGGAGTAAACACTGTAATAAATATATTTTTTGTGTTACTTCTAAGAGAAAGAGTA 3300  
QY TTGTTATGTTCTCCTAAGTCTGTTGATTAAGTATTTAAAGTATTTCAATTTAAACATT 3360  
Db 3301 TTGTTATGTTCTCCTAAGTCTGTTGATTAAGTATTTAAAGTATTTCAATTTAAACATT 3360  
QY GCAAAATTTATTTATTTATTTTCTTTTGGAGTGGAGTCTGCTTCTCACCAGG 3420  
|||||

Db 3361 GCAAAATTTATTTTATTTATTTTCTTTTGGAGTGGAGTCTTGTCTGACCCAGG 3420  
QY CTGAGTGCAGTGGAGTGATCTGCTCAGTGCACCTCCGCTTCTGGTTCAGCGAT 3480  
Db 3421 CTGAGTGCAGTGGAGTGATCTGCTCAGTGCACCTCCGCTTCTGGTTCAGCGAT 3480  
QY TCTCGTGCCTCAGCTTCTGTAGTGTGAATATACAGCAGGTGCCACCATGCCGACTA 3540  
Db 3481 TCTCGTGCCTCAGCTTCTGTAGTGTGAATATACAGCAGGTGCCACCATGCCGACTA 3540  
QY ATTTTTTTTTTATTTTATTTAGTAGAGAGGGGTTTACACATGTTGGCAGGCTGGTATCAAC 3600  
Db 3541 ATTTTTTTTTTATTTTATTTAGTAGAGAGGGGTTTACACATGTTGGCAGGCTGGTATCAAC 3600  
QY TCCTGACCTCAAGAGATCCACTCGCTTGGCTTCCCAAGTGTGGGATTTACAGGCTTGA 3660  
Db 3601 TCCTGACCTCAAGAGATCCACTCGCTTGGCTTCCCAAGTGTGGGATTTACAGGCTTGA 3660  
QY GCCACCAGCCCGCTAAACATTTGCAAAATTTAAATGAGAGTTTTTAAAAATTTAAATAATG 3720  
Db 3661 GCCACCAGCCCGCTAAACATTTGCAAAATTTAAATGAGAGTTTTTAAAAATTTAAATAATG 3720  
QY ACTGCCCTGTTTCTGTTTTAGTATGTAATCCTCAGTTCCTACCTTTGCACCTGTCTGCC 3780  
Db 3721 ACTGCCCTGTTTCTGTTTTAGTATGTAATCCTCAGTTCCTACCTTTGCACCTGTCTGCC 3780  
QY ACTTAGTTTGGTTATATAGTCAATTAACCTTGAATTTGGTCTGTATAGTCTAGACTTTAAAT 3840  
Db 3781 ACTTAGTTTGGTTATATAGTCAATTAACCTTGAATTTGGTCTGTATAGTCTAGACTTTAAAT 3840  
QY TTAAGTTTTTCTACAAGGGGAGAAAAAGTGTAAAAATTTTTTAAAAATATGTTTTCCAGGACA 3900  
Db 3841 TTAAGTTTTTCTACAAGGGGAGAAAAAGTGTAAAAATTTTTTAAAAATATGTTTTCCAGGACA 3900  
QY CTTCACTTCCAAGTCAGGTAGTTCATCTAGTTTGGTTCAGCCAAAGGACTCAAGGACTG 3960  
Db 3901 CTTCACTTCCAAGTCAGGTAGTTCATCTAGTTTGGTTCAGCCAAAGGACTCAAGGACTG 3960  
QY AATTGTTTTTAAATAAGGCTTTTCTGTTCTGGGAGCGGCTTCAATTAATAATTTCTCTA 4020  
Db 3961 AATTGTTTTTAAATAAGGCTTTTCTGTTCTGGGAGCGGCTTCAATTAATAATTTCTCTA 4020  
QY AAACCTTGATGTTTATAGATTTAAGCAAGACTTTTTTCTCTCTCTCATGAGTGTGAAAT 4080  
Db 4021 AAACCTTGATGTTTATAGATTTAAGCAAGACTTTTTTCTCTCTCTCATGAGTGTGAAAT 4080  
QY TTAATGCACACGCTGATGTGGCTAACAAGTTTATTTTAAAGAAATGTTTAGAAATGCTGT 4140  
Db 4081 TTAATGCACACGCTGATGTGGCTAACAAGTTTATTTTAAAGAAATGTTTAGAAATGCTGT 4140  
QY TGCTTCAGGTTCTTAAAAATCACTCAGCACTCCAACTTCTTAATCAAAATTTTGGAGACTTA 4200  
Db 4141 TGCTTCAGGTTCTTAAAAATCACTCAGCACTCCAACTTCTTAATCAAAATTTTGGAGACTTA 4200  
QY ACAGCATTTGCTGTGTTGAACATATAAAAAAGCAGCGGATCTTTTCCATCTAATTTCCGCA 4260  
Db 4201 ACAGCATTTGCTGTGTTGAACATATAAAAAAGCAGCGGATCTTTTCCATCTAATTTCCGCA 4260  
QY AAAATTGATCATTTGCAAGTCAAAACTATAGCCATATCCAAATCTTTTCCCTCCCAA 4320  
Db 4261 AAAATTGATCATTTGCAAGTCAAAACTATAGCCATATCCAAATCTTTTCCCTCCCAA 4320  
QY GAGTTCAGTGTCTACATGTAGACTATTCCTTTTCTGTATAAAGTCTCAGTCTAGGATTT 4380  
Db 4321 GAGTTCAGTGTCTACATGTAGACTATTCCTTTTCTGTATAAAGTCTCAGTCTAGGATTT 4380  
QY CAAGTCACCACTTATTTTACATTTTAGTCATGCAAGATTTCAAGTAGTTTTCGAATAAGT 4440  
Db 4381 CAAGTCACCACTTATTTTACATTTTAGTCATGCAAGATTTCAAGTAGTTTTCGAATAAGT 4440  
QY ACTTATCTTTTATTTGTAATAATTTAGTCTGCTGATCAAAAGCATTTGCTTAATTTTGGAG 4500  
Db 4441 ACTTATCTTTTATTTGTAATAATTTAGTCTGCTGATCAAAAGCATTTGCTTAATTTTGGAG 4500  
|||||

Qy 4501 AACTGGTTTATAGCAATTTACAACTAAATCCAGTTAAATTAATAGCTTTATATGCC 4560  
Db 4501 AACTGGTTTATAGCAATTTACAACTAAATCCAGTTAAATTAATAGCTTTATATGCC 4560  
Qy 4561 TTTCCTGCTACATTTGGTGTTCCTCCCTGTCCTTTGATTAAGGCTAAGGTAGGTAAG 4620  
Db 4561 TTTCCTGCTACATTTGGTGTTCCTCCCTGTCCTTTGATTAAGGCTAAGGTAGGTAAG 4620  
Qy 4621 ANNGGCTGAGTGTATATATGTCATTTGGCCCTGTCGTATATATATATATTTGTTAT 4680  
Db 4621 ANNGGCTGAGTGTATATATGTCATTTGGCCCTGTCGTATATATATATTTGTTAT 4680  
Qy 4681 TTTTGTCTTATATATTTACATTTTCAGTAGTGTGTTTTGTTGTTCCATTTTAGGGAT 4740  
Db 4681 TTTTGTCTTATATTTACATTTTCAGTAGTGTGTTTTGTTGTTCCATTTTAGGGAT 4740  
Qy 4741 AAAATTTGATTTTGAACATGATGAATGGAGACTACGCCCCAGCAATAGTTTCACATGATA 4800  
Db 4741 AAAATTTGATTTTGAACATGATGAATGGAGACTACGCCCCAGCAATAGTTTCACATGATA 4800  
Qy 4801 TACCCCTTTAAACCCCAATCATTTGTTTATTTCCCTGATTACACAGCTGTTGAATGGGAAA 4860  
Db 4801 TACCCCTTTAAACCCCAATCATTTGTTTATTTCCCTGATTACACAGCTGTTGAATGGGAAA 4860  
Qy 4861 GGGGCTAGTATATACAGTATATATCTAGTATGATGATGATATATATATATGCTGTTAGAGAA 4920  
Db 4861 GGGGCTAGTATATACAGTATATATCTAGTATGATGATGATATATATATATGCTGTTAGAGAA 4920  
Qy 4921 ATGAATAAATAGGGCTGGGCTCAGTGGCTCAGCCCTGTAATCCACAGACTTTGGGAGG 4980  
Db 4921 ATGAATAAATAGGGCTGGGCTCAGTGGCTCAGCCCTGTAATCCACAGACTTTGGGAGG 4980  
Qy 4981 CTGAGGAGGTGGATCAGAGTCAAGGATCGAGACCATCTGGCTAACAGGTGAAC 5040  
Db 4981 CTGAGGAGGTGGATCAGAGTCAAGGATCGAGACCATCTGGCTAACAGGTGAAC 5040  
Qy 5041 CCCGCTCTACTAAAAACAGAAAAATTAGCCGGCGTGGTGGCCGGCCCTGTAGTCCCA 5100  
Db 5041 CCCGCTCTACTAAAAACAGAAAAATTAGCCGGCGTGGTGGCCGGCCCTGTAGTCCCA 5100  
Qy 5101 GCTACTCGGGAGGCTGAGCGAGGAGAAATGTTGTGNAACCCGGGAGGAGCTTGCAGTGA 5160  
Db 5101 GCTACTCGGGAGGCTGAGCGAGGAGAAATGTTGTGNAACCCGGGAGGAGCTTGCAGTGA 5160  
Qy 5161 GCCGAGATCTCGCCACTGCACCTCCAGCTGGGCAACAGCAAGACTCTGTCTCAAAAAA 5220  
Db 5161 GCCGAGATCTCGCCACTGCACCTCCAGCTGGGCAACAGCAAGACTCTGTCTCAAAAAA 5220  
Qy 5221 AAAAAAAG 5232  
Db 5221 AAAAAAAG 5232

RESULT 2  
US-08-800-929A-3  
; Sequence 3, Application US/08800929A  
; Patent No. 6133437  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G  
; APPLICANT: Mackenzie, Alexander E  
; APPLICANT: Liston, Peter  
; APPLICANT: Baird, Stephen  
; APPLICANT: Tsang, Benjamin K  
; APPLICANT: Pratt, Christine  
; TITLE OF INVENTION: DETECTION AND MODULATION OF  
; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Clark & Elbing LLP  
; STREET: 176 Federal Street  
; CITY: Boston

STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/800,929A  
FILING DATE: 13-FEB-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/030,590  
FILING DATE: 14-NOV-1996  
APPLICATION NUMBER: 60/017,354  
FILING DATE: 26-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Bieker-Brady, Kristina  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 07891/009001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-428-0200  
TELEFAX: 617-428-7045  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5232 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
FEATURE:  
NAME/KEY: Other  
LOCATION: 1...5232  
OTHER INFORMATION: N at 4622 and 4633 can be A, G, T or C.  
US-08-800-929A-3  
Query Match 100.0%; Score 5232; DB 3; Length 5232;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAAAGGTGGACAACTCCTATTTTCAAGAGAAAGATGACTTTTAAACAGTTTGAAGGATCT 60  
Db 1 GAAAGGTGGACAACTCCTATTTTCAAGAGAAAGATGACTTTTAAACAGTTTGAAGGATCT 60  
Qy 61 AAAAATCTGTGTACCTGCAGACATCAATAGGAAGAGAAATTTGTAGAGAGTTTAATAGA 120  
Db 61 AAAAATCTGTGTACCTGCAGACATCAATAGGAAGAGAAATTTGTAGAGAGTTTAATAGA 120  
Qy 121 TAAAAACTTTTGTCTAATTTTCCAAAGTGTAGTCTCTGTTTCCAGCATCAACACTGGCAGGA 180  
Db 121 TAAAAACTTTTGTCTAATTTTCCAAAGTGTAGTCTCTGTTTCCAGCATCAACACTGGCAGGA 180  
Qy 181 GCAGGGTTTCTTATATCTGTTGAAGAGATACCGTGCAGGCTGCTTTAGTTGTCATGACGT 240  
Db 181 GCAGGGTTTCTTATATCTGTTGAAGAGATACCGTGCAGGCTGCTTTAGTTGTCATGACGT 240  
Qy 241 GTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAAGACACAGAGAAAGTATCCCAAT 300  
Db 241 GTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAAGACACAGAGAAAGTATCCCAAT 300  
Qy 301 TGCAGATTTATCAACGGCTTTTATCTTGAAAAATAGTGGCCAGCAGCTACAAATTTCTGT 360  
Db 301 TGCAGATTTATCAACGGCTTTTATCTTGAAAAATAGTGGCCAGCAGCTACAAATTTCTGT 360  
Qy 361 ATCCAGAAATGGTCACTACAAAGTTGAAACATCTCTGGGAAGCAGAGATCATTTTGCCTTA 420  
Db 361 ATCCAGAAATGGTCACTACAAAGTTGAAACATCTCTGGGAAGCAGAGATCATTTTGCCTTA 420  
Qy 421 GACAGGCCATCTGAGACACATGCACACTATCTTTTGAAGACTGGGCAGCTTGTAGATATA 480  
Db 421 GACAGGCCATCTGAGACACATGCACACTATCTTTTGAAGACTGGGCAGCTTGTAGATATA 480





Db 2641 TTTCAAAATAGTATTTCTGATTTTGTAAATGAAATATAAATATGCTCAGATCTTCCC 2700  
Qy 2701 AATTAATTAAGTAAAGGATTCATCCCTTAATCCCTGCTAGTTAAAGCGCTGCTTAAGTCACTTT 2760  
Db 2701 AATTAATTAAGTAAAGGATTCATCCCTTAATCCCTGCTAGTTAAAGCGCTGCTTAAGTCACTTT 2760  
Qy 2761 ACTAAAGATCTTTGTTAACTCAGTATTTTAAACATCTGTCAGCTTATGTAAGGTAAGT 2820  
Db 2761 ACTAAAGATCTTTGTTAACTCAGTATTTTAAACATCTGTCAGCTTATGTAAGGTAAGT 2820  
Qy 2821 AGAAGCATGTTGTACACTGCTGTAGTATATAGTGACAGCTTTCCATGTTGAGATTTCTCA 2880  
Db 2821 AGAAGCATGTTGTACACTGCTGTAGTATATAGTGACAGCTTTCCATGTTGAGATTTCTCA 2880  
Qy 2881 TATCATCTGTATCTTAAAGTTTTCATGTGAGTTTAAACCGTTAGGATGATTAAGATGTAT 2940  
Db 2881 TATCATCTGTATCTTAAAGTTTTCATGTGAGTTTAAACCGTTAGGATGATTAAGATGTAT 2940  
Qy 2941 ATAGACAAAATGTTAAGTCTTTTCTCTACCTACATTTGTTTCTGCTGCTAGTAAATAGTA 3000  
Db 2941 ATAGACAAAATGTTAAGTCTTTTCTCTACCTACATTTGTTTCTGCTGCTAGTAAATAGTA 3000  
Qy 3001 ATATGTCAGAAAGAAAGAAATAGTCTTTAAATATATTTTAAACACCTTTGAATTAAG 3120  
Db 3001 ATATGTCAGAAAGAAAGAAATAGTCTTTAAATATATTTTAAACACCTTTGAATTAAG 3120  
Qy 3121 AATCAGTAGGATTAATACTAGAAAGTTTAAATGCTCATAGAGCTCCAGGGTTTACAT 3180  
Db 3121 AATCAGTAGGATTAATACTAGAAAGTTTAAATGCTCATAGAGCTCCAGGGTTTACAT 3180  
Qy 3181 TACAGATCTTCACACAAACCCATTTAGAGTGAGTAAGGCATGTTACTACAGAGAA 3240  
Db 3181 TACAGATCTTCACACAAACCCATTTAGAGTGAGTAAGGCATGTTACTACAGAGAA 3240  
Qy 3241 AGTTTGAGAGTAAACTCTAAATAATATATTTTGTGTTCTTCTAAGAGAAAGAGTA 3300  
Db 3241 AGTTTGAGAGTAAACTCTAAATAATATATTTTGTGTTCTTCTAAGAGAAAGAGTA 3300  
Qy 3301 TTGTTATGTTCTCCTAATCTCTGTTGATTAATCTTAAAGTGATTAATCAATTTAAACATTT 3360  
Db 3301 TTGTTATGTTCTCCTAATCTCTGTTGATTAATCTTAAAGTGATTAATCAATTTAAACATTT 3360  
Qy 3361 GCAAAATTTATTTTATTTTAAATTTCTTTTGTAGATGGAGTCTTGCTGTCCACAGG 3420  
Db 3361 GCAAAATTTATTTTATTTTAAATTTCTTTTGTAGATGGAGTCTTGCTGTCCACAGG 3420  
Qy 3421 CTGGAGTCAGTGGAGTATCTCTGCTCAGTCAACCTCCGCTTCTGGGTTCAAGCGAT 3480  
Db 3421 CTGGAGTCAGTGGAGTATCTCTGCTCAGTCAACCTCCGCTTCTGGGTTCAAGCGAT 3480  
Qy 3481 TCTGCTGCTCAGCTTCTGAGTCTGAGTGGATTTAGAGCAGGTGCCACCATGCCCGACTA 3540  
Db 3481 TCTGCTGCTCAGCTTCTGAGTCTGAGTGGATTTAGAGCAGGTGCCACCATGCCCGACTA 3540  
Qy 3541 ATTTTATTTTATTTTATTTAGTAGAGGGGTTTCAACATGTTGGCAGGCTGGTATCAAC 3600  
Db 3541 ATTTTATTTTATTTTATTTAGTAGAGGGGTTTCAACATGTTGGCAGGCTGGTATCAAC 3600  
Qy 3601 TCCTGACCTCAAGAGATCCATCGCTTTCGCTCCCAAGTCTGGGATTTACAGGCTTGA 3660  
Db 3601 TCCTGACCTCAAGAGATCCATCGCTTTCGCTCCCAAGTCTGGGATTTACAGGCTTGA 3660  
Qy 3661 GCCACCGCCGGCTAAACATTTGCAAAATTTAATGAGAGTTTAAATAATG 3720  
Db 3661 GCCACCGCCGGCTAAACATTTGCAAAATTTAATGAGAGTTTAAATAATG 3720  
Qy 3721 ACTGCCCTGTTCTGTTTATGATGTAATCTCAGTCTTCCACTTTGCACTGTCTGCC 3780  
Db 3721 ACTGCCCTGTTCTGTTTATGATGTAATCTCAGTCTTCCACTTTGCACTGTCTGCC 3780

Db 3721 ACTGCCCTGTTCTGTTTATGATGTAATCTCAGTCTTCCACTTTGCACTGTCTGCC 3780  
Qy 3781 ACTTAGTTTGGTTATATAGTCAATTAACCTTGAATTTGGTCTGTATAGTCTAGACTTTAAAT 3840  
Db 3781 ACTTAGTTTGGTTATATAGTCAATTAACCTTGAATTTGGTCTGTATAGTCTAGACTTTAAAT 3840  
Qy 3841 TTAAGTTTCTTACAAGGGGAGAAAGTGTAAATTTTAAATATGTTTTCAGGACA 3900  
Db 3841 TTAAGTTTCTTACAAGGGGAGAAAGTGTAAATTTTAAATATGTTTTCAGGACA 3900  
Qy 3901 CTTCACTTCCCAAGTCAGGTAGTCAATCTAGTCTTCCAGGAGCGCACTTCATTAATAATTTCTTA 3960  
Db 3901 CTTCACTTCCCAAGTCAGGTAGTCAATCTAGTCTTCCAGGAGCGCACTTCATTAATAATTTCTTA 3960  
Qy 3961 AATGTTTAAACATAAGGCTTTTCTGTTGGGAGCGCACTTCATTAATAATTTCTTA 4020  
Db 3961 AATGTTTAAACATAAGGCTTTTCTGTTGGGAGCGCACTTCATTAATAATTTCTTA 4020  
Qy 4021 AAACCTGATGTTAGAGTTAAGCAAGCTTTTCTGTTGGGAGCGCACTTCATTAATAATTTCTTA 4080  
Db 4021 AAACCTGATGTTAGAGTTAAGCAAGCTTTTCTGTTGGGAGCGCACTTCATTAATAATTTCTTA 4080  
Qy 4081 TTAATGCAACAAGCTGATGCTGAACAAGTTTATTTTAAAGAAATTTTAGAAATGCTGT 4140  
Db 4081 TTAATGCAACAAGCTGATGCTGAACAAGTTTATTTTAAAGAAATTTTAGAAATGCTGT 4140  
Qy 4141 TGCCTCAGGTTCTTAAATCACTCAGCACTCCAACTTCTAATCAAAATTTTGGAGACTTA 4200  
Db 4141 TGCCTCAGGTTCTTAAATCACTCAGCACTCCAACTTCTAATCAAAATTTTGGAGACTTA 4200  
Qy 4201 ACAGCATTTGCTGTTTGAACATAAAAAAGCACCGGATCTTTTCCATCTAATTTCCGCA 4260  
Db 4201 ACAGCATTTGCTGTTTGAACATAAAAAAGCACCGGATCTTTTCCATCTAATTTCCGCA 4260  
Qy 4261 AAAATGATCATTTGCAAGTCAAAACATATAGCCATATCCAACTTCTTCCCTCCCAA 4320  
Db 4261 AAAATGATCATTTGCAAGTCAAAACATATAGCCATATCCAACTTCTTCCCTCCCAA 4320  
Qy 4321 GAGTCTCAGTCTTACATGATGACTATTTCTTCTGTATATAAGTCTTCACTAGGATTT 4380  
Db 4321 GAGTCTCAGTCTTACATGATGACTATTTCTTCTGTATATAAGTCTTCACTAGGATTT 4380  
Qy 4381 CAAGTCACCATTAATTTACATTTTAGTCATGCAAAAGTTCAGTAGTTTTCGCAATAGT 4440  
Db 4381 CAAGTCACCATTAATTTACATTTTAGTCATGCAAAAGTTCAGTAGTTTTCGCAATAGT 4440  
Qy 4441 ACTTATCTTTTATTTGTAATAATTTAGTCTGCTGATCAAAAGCATTTCTTAATTTTGGAG 4500  
Db 4441 ACTTATCTTTTATTTGTAATAATTTAGTCTGCTGATCAAAAGCATTTCTTAATTTTGGAG 4500  
Qy 4501 AACTGGTTTTAGCATTTACAACTAAATTCAGTTTAAATTAATAGCTTTATATGCC 4560  
Db 4501 AACTGGTTTTAGCATTTACAACTAAATTCAGTTTAAATTAATAGCTTTATATGCC 4560  
Qy 4561 TTTCCTGCTACATTTGGTTTTTTTCCCTTGTCCCTTGTGATTACGGGCTAAGGTAGGTAAG 4620  
Db 4561 TTTCCTGCTACATTTGGTTTTTTTCCCTTGTCCCTTGTGATTACGGGCTAAGGTAGGTAAG 4620  
Qy 4621 ANNGGTCAGTGTAGTATATAATGATTTGGCCCTGTGTATTTATGATATTTTGTAT 4680  
Db 4621 ANNGGTCAGTGTAGTATATAATGATTTGGCCCTGTGTATTTATGATATTTTGTAT 4680  
Qy 4681 TTTTGTCTTATATTTTACATTTTACATTTTACATTTTACATTTTACATTTTACATTTTACATTT 4740  
Db 4681 TTTTGTCTTATATTTTACATTTTACATTTTACATTTTACATTTTACATTTTACATTTTACATTT 4740  
Qy 4741 AAAATTTGATTTTGAACATATGAATGGAGACTACCGCCCGGAGCATTTTTCACATGATA 4800  
Db 4741 AAAATTTGATTTTGAACATATGAATGGAGACTACCGCCCGGAGCATTTTTCACATGATA 4800  
Qy 4801 TACCTTTTAAACCGAATCATTTGTTTATTTTCTGATTTACAGGTTGATTTGGGAAA 4860  
Db 4801 TACCTTTTAAACCGAATCATTTGTTTATTTTCTGATTTACAGGTTGATTTGGGAAA 4860



Db 1141 ATCTTCCAAAATCCTATGGTACAGAGAGCTATACGAATGGGGTTCAGTTTCAAGACAAAT 1200  
Qy 1201 AAGAAAATAATGGAGAAAAAATCAGATATCTGGAGCAACTATAAATCACTTCAGGTT 1260  
Db 1201 AAGAAAATAATGGAGAAAAAATCAGATATCTGGAGCAACTATAAATCACTTCAGGTT 1260  
Qy 1261 CTGGTTGCAGATCTAGTGAATGCTCAGAAAGACAGTATGCAAGATGAGTCAAGTCAGACT 1320  
Db 1261 CTGGTTGCAGATCTAGTGAATGCTCAGAAAGACAGTATGCAAGATGAGTCAAGTCAGACT 1320  
Qy 1321 TCATTACAGAAAGAGATTAGTACCTGAGAGCAGCTAGGCGCTGCAAGAGAGAGAGCTT 1380  
Db 1321 TCATTACAGAAAGAGATTAGTACCTGAGAGCAGCTAGGCGCTGCAAGAGAGAGAGCTT 1380  
Qy 1381 TGCAAAATCTGTATGGATAGAAAATTTGCTATCGTTTTTGTCTGTTGGACATCTAGTC 1440  
Db 1381 TGCAAAATCTGTATGGATAGAAAATTTGCTATCGTTTTTGTCTGTTGGACATCTAGTC 1440  
Qy 1441 ACTTGTAAACAATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGTCATTA 1500  
Db 1441 ACTTGTAAACAATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGTCATTA 1500  
Qy 1501 TTCAAGCAAAAATTTTTATGCTCTTAATCTAACCTATAGTAGGCACTGTTATGTTGTTCT 1560  
Db 1501 TTCAAGCAAAAATTTTTATGCTCTTAATCTAACCTATAGTAGGCACTGTTATGTTGTTCT 1560  
Qy 1561 TATTACCTGATTTGAATGTGTGATGTGAACCTGACTTTAAGTAATCAGGATTTCAATCCAT 1620  
Db 1561 TATTACCTGATTTGAATGTGTGATGTGAACCTGACTTTAAGTAATCAGGATTTGAATCCAT 1620  
Qy 1621 TAGCAATTTGCTACCAAGTAGGAAAAAATGTACATGCGAGTGTGTTAGTTGGCAATATA 1680  
Db 1621 TAGCAATTTGCTACCAAGTAGGAAAAAATGTACATGCGAGTGTGTTAGTTGGCAATATA 1680  
Qy 1681 ATCTTTGAATTTCTGATTTTTCAGGATTTAGCTGTATTAATCCATTTTTTTTACTGTTA 1740  
Db 1681 ATCTTTGAATTTCTGATTTTTCAGGATTTAGCTGTATTAATCCATTTTTTTTACTGTTA 1740  
Qy 1741 TTTAATTTGAAACCATAGACTAAGATAAGAGCATCATACTATAACTGAACACAAATGTGT 1800  
Db 1741 TTTAATTTGAAACCATAGACTAAGATAAGAGCATCATACTATAACTGAACACAAATGTGT 1800  
Qy 1801 ATTCAATGATACATGATTTAATTTCTAAGTGAAGTGAATTAATCACTCTGGAATTTTTAT 1860  
Db 1801 ATTCAATGATACATGATTTAATTTCTAAGTGAAGTGAATTAATCACTCTGGAATTTTTAT 1860  
Qy 1861 TCCTTTTCAGATAGGCTTAACAAATGGAGCTTCTGTATATAAATGTGGAGATTAGAGTTA 1920  
Db 1861 TCCTTTTCAGATAGGCTTAACAAATGGAGCTTCTGTATATAAATGTGGAGATTAGAGTTA 1920  
Qy 1921 ATCTCCCAATCACATAATTTGTTGTGTGAAAGGAATAAATGTTCCATGCTGGTG 1980  
Db 1921 ATCTCCCAATCACATAATTTGTTGTGTGAAAGGAATAAATGTTCCATGCTGGTG 1980  
Qy 1981 GAAAGATAGAGATTTTATAGGTTGGTTGTGTTGTTTATAGGATCTGTCCATTTTCT 2040  
Db 1981 GAAAGATAGAGATTTTATAGGTTGGTTGTGTTGTTTATAGGATCTGTCCATTTTCT 2040  
Qy 2041 TTTAAAGTTATAAACACCTACTTGTGCAATTAATTTTTTAAAGTATTTGCCATTTTTG 2100  
Db 2041 TTTAAAGTTATAAACACCTACTTGTGCAATTAATTTTTTAAAGTATTTGCCATTTTTG 2100  
Qy 2101 AAAGCGTATTTAATGATAGATACTATCGAGCCAACTGTGACTGACATGGAAAGATGTCA 2160  
Db 2101 AAAGCGTATTTAATGATAGATACTATCGAGCCAACTGTGACTGACATGGAAAGATGTCA 2160  
Qy 2161 AAGATATGTTAAGTGTAAATTCAGAGTGGCAAAACACTATGATAGTCTGAGCCAGATCA 2220  
Db 2161 AAGATATGTTAAGTGTAAATTCAGAGTGGCAAAACACTATGATAGTCTGAGCCAGATCA 2220  
Qy 2221 AAGTATGATCTTTTATATGCTAGAACAAAGATTTGGAAGATATACCCAACTG 2280  
Db 2221 AAGTATGATCTTTTATATGCTAGAACAAAGATTTGGAAGATATACCCAACTG 2280

Qy 2281 TTAAATGTGGTTTCTTTCGGGAGGGGGGATTTGGGGAGGGCCCCCAGAGGGTTTTTA 2340  
Db 2281 TTAAATGTGGTTTCTTTCGGGAGGGGGGATTTGGGGAGGGCCCCCAGAGGGTTTTTA 2340  
Qy 2341 TAGGGCCCTTTTCTACTTTCTACTTTTCTACTTTTCTGTTCTGTTCTGNAATTTTTTAAGTAT 2400  
Db 2341 TAGGGCCCTTTTCTACTTTTCTACTTTTCTACTTTTCTGTTCTGTTCTGNAATTTTTTAAGTAT 2400  
Qy 2401 GTATTACTTTTGTAAATCAGAAATTTTGAAGAGTATTTTGTGCTGATTTAAAGCTTAGGCAT 2460  
Db 2401 GTATTACTTTTGTAAATCAGAAATTTTGAAGAGTATTTTGTGCTGATTTAAAGCTTAGGCAT 2460  
Qy 2461 GTTCAAAAGCGCTGCACAAACTACTTATCACTCAGCTTTAGTTTTCTTAATCCAAGAGCA 2520  
Db 2461 GTTCAAAAGCGCTGCACAAACTACTTATCACTCAGCTTTAGTTTTCTTAATCCAAGAGCA 2520  
Qy 2521 GGGCAGTTAAACCTTTTGGTGCCAAATGTGAATGTAAATGATTTTATGTTTTTCTGCTT 2580  
Db 2521 GGGCAGTTAAACCTTTTGGTGCCAAATGTGAATGTAAATGATTTTATGTTTTTCTGCTT 2580  
Qy 2581 TGTGATGAAAAATATTTCTGAGTGGTAGTTTGTGACAGGTAGACCATGCTTATCTTG 2640  
Db 2581 TGTGATGAAAAATATTTCTGAGTGGTAGTTTGTGACAGGTAGACCATGCTTATCTTG 2640  
Qy 2641 TTTCAAAATAAAGTATTTCTGATTTTGTAAAAATGAATATAAATATGCTCAGATCTTCC 2700  
Db 2641 TTTCAAAATAAAGTATTTCTGATTTTGTAAAAATGAATATAAATATGCTCAGATCTTCC 2700  
Qy 2701 AATTAAATTAGTAAGGATTCATCTTAATCTCTGCTAGTTTAAAGCTGCTTAAGTCACATT 2760  
Db 2701 AATTAAATTAGTAAGGATTCATCTTAATCTCTGCTAGTTTAAAGCTGCTTAAGTCACATT 2760  
Qy 2761 ACTAAAGATCTTTGTTAACTCAGTATTTTAAACATCTGCAGCTTATGTAGGTAAGT 2820  
Db 2761 ACTAAAGATCTTTGTTAACTCAGTATTTTAAACATCTGCAGCTTATGTAGGTAAGT 2820  
Qy 2821 AGAAGCATGTTTGTACACTGCTTGTAGTTATAGTGACAGCTTTCATGTTGAGATTTCTCA 2880  
Db 2821 AGAAGCATGTTTGTACACTGCTTGTAGTTATAGTGACAGCTTTCATGTTGAGATTTCTCA 2880  
Qy 2881 TATCATCTGTGATCTTAAAGTTTCAATGAGTTTACCGTTAGGATGATTAAGATGAT 2940  
Db 2881 TATCATCTGTGATCTTAAAGTTTCAATGAGTTTACCGTTAGGATGATTAAGATGAT 2940  
Qy 2941 ATAGCAAAAATGTTAAGTCTTCTCTACCTACATTTGTTTCTGCTAGTAAATAGTA 3000  
Db 2941 ATAGCAAAAATGTTAAGTCTTCTCTACCTACATTTGTTTCTGCTAGTAAATAGTA 3000  
Qy 3001 GTAGATCTTCTGAAATAAATGTTCTCTCAAGATCCTTAAACCCCTTTGGAAATTTATAA 3060  
Db 3001 GTAGATCTTCTGAAATAAATGTTCTCTCAAGATCCTTAAACCCCTTTGGAAATTTATAA 3060  
Qy 3061 AATATTGCAAGAAAAGAAAGATAGTTGTTTAAATATTTTTTAAACACACTTGAATAG 3120  
Db 3061 AATATTGCAAGAAAAGAAAGATAGTTGTTTAAATATTTTTTAAACACACTTGAATAG 3120  
Qy 3121 AATCAGTAGGGTATAAATGAGTTTAAATGCTCATAGAACGCTCCAGGTTTACAT 3180  
Db 3121 AATCAGTAGGGTATAAATGAGTTTAAATGCTCATAGAACGCTCCAGGTTTACAT 3180  
Qy 3181 TACAAGATTTCTACAAACAAACCCATTTGAGAGGTGAGTAAGGCATGTTTACTACAGAGAA 3240  
Db 3181 TACAAGATTTCTACAAACAAACCCATTTGAGAGGTGAGTAAGGCATGTTTACTACAGAGAA 3240  
Qy 3241 AGTTTGAGAGTAAACTGTAATAAATATATTTTGTGTTACTTCTTAAGAGAAAGATA 3300  
Db 3241 AGTTTGAGAGTAAACTGTAATAAATATATTTTGTGTTACTTCTTAAGAGAAAGATA 3300  
Qy 3301 TTGTTATCTTCTTAACTTCTGTTGATTTACTTAAAGTGAATTCATTTAAACATTT 3360  
Db 3301 TTGTTATCTTCTTAACTTCTGTTGATTTACTTAAAGTGAATTCATTTAAACATTT 3360



ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/511.485  
FILING DATE: 04-AUG-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 07540/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2540 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: DNA (genomic)  
US-08-511-485-3

Query Match 38.0%; Score 1990; DB 2; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAAGGTGGCAAGTCTCTATTTTCAAGAGAGATGACTTTTAAACAGTCTTTGAAGGATCT 60  
Db 1 GAAAGGTGGCAAGTCTCTATTTTCAAGAGAGATGACTTTTAAACAGTCTTTGAAGGATCT 60  
Qy 61 AAAAGTGTGTACCTGCAGACATCAATTAAGGAAGAAGATTTGTAGAAGAGTTTAATAGA 120  
Db 61 AAAAGTGTGTACCTGCAGACATCAATTAAGGAAGAAGATTTGTAGAAGAGTTTAATAGA 120  
Qy 121 TTAAGAACTTTTGTAAATTTTCAAGTGGTAGTCTCTGTTTCAAGTCAACACTGGCAGCA 180  
Db 121 TTAAGAACTTTTGTAAATTTTCAAGTGGTAGTCTCTGTTTCAAGTCAACACTGGCAGCA 180  
Qy 181 GCAGGGTTCTTTTACCTGAGAGAGATACCGTGCAGTCTTTAGTTGTCATGCACT 240  
Db 181 GCAGGGTTCTTTTACCTGAGAGAGATACCGTGCAGTCTTTAGTTGTCATGCACT 240  
Qy 241 GTAGATAGATGGCAATATGGAGACTTCAGAGTGGAAACACAGAGAAAGTATCCCAAT 300  
Db 241 GTAGATAGATGGCAATATGGAGACTTCAGAGTGGAAACACAGAGAAAGTATCCCAAT 300  
Qy 301 TGCAGATTTATCAAGCGCTTTTATCTTGAAGTGTGCGCAGCTACAAATTTCTGTT 360  
Db 301 TGCAGATTTATCAAGCGCTTTTATCTTGAAGTGTGCGCAGCTACAAATTTCTGTT 360  
Qy 361 ATCCAGAAATGGTACAGTACAAAGTGTAAAGTATCTCTGGAAGCAGAGATCATTTTGCCTTA 420  
Db 361 ATCCAGAAATGGTACAGTACAAAGTGTAAAGTATCTCTGGAAGCAGAGATCATTTTGCCTTA 420  
Qy 421 GACAGGCCATCTGAGACACATGCAGACTATCTTTTGAAGTGGCAGGTTGTAGATATA 480  
Db 421 GACAGGCCATCTGAGACACATGCAGACTATCTTTTGAAGTGGCAGGTTGTAGATATA 480  
Qy 481 TCAGACACCATATACCCGAGGAACCTGCCATGTATGTAGTGAAGAGCTPAGATTAAGTCC 540  
Db 481 TCAGACACCATATACCCGAGGAACCTGCCATGTATGTAGTGAAGAGCTPAGATTAAGTCC 540  
Qy 541 TTTCAGAACTGGCCAGACTATGCTACACTAACCCCAAGAGAGTTAGCAAGTCTGGACTC 600  
Db 541 TTTCAGAACTGGCCAGACTATGCTACACTAACCCCAAGAGAGTTAGCAAGTCTGGACTC 600  
Qy 601 TACTACAGGTATTTGGTACCAAGTGCAGTCTTTTGTGTTGGTGGAAACTGAAAAAT 660  
Db 601 TACTACAGGTATTTGGTACCAAGTGCAGTCTTTTGTGTTGGTGGAAACTGAAAAAT 660

Db 601 TACTACAGGTATTTGGTACCAAGTGCAGTCTTTTGTGTTGGTGGAAACTGAAAAAT 660  
Qy 661 TGGGAACCTTGTGATCGTCCGTGTCAGAACACAGCGACACTTTCCCTAAATGCTCTTT 720  
Db 661 TGGGAACCTTGTGATCGTCCGTGTCAGAACACAGCGACACTTTCCCTAAATGCTCTTT 720  
Qy 721 GTTTTGGGCCGGAATCTTAATATTCGAAGTGAATCTGATGCTGTGAGTCTGATAGGAAT 780  
Db 721 GTTTTGGGCCGGAATCTTAATATTCGAAGTGAATCTGATGCTGTGAGTCTGATAGGAAT 780  
Qy 781 TTCCCAAAATTCACAAATCTTCCCAAGAAATCCATCCATGGCAGATATGAAGCAGGATC 840  
Db 781 TTCCCAAAATTCACAAATCTTCCCAAGAAATCCATCCATGGCAGATATGAAGCAGGATC 840  
Qy 841 TTTTACTTTTGGGACATGGATATACCTCAGTTTAAAGAGGACAGCTTGCAGAGCTGATTT 900  
Db 841 TTTTACTTTTGGGACATGGATATACCTCAGTTTAAAGAGGACAGCTTGCAGAGCTGATTT 900  
Qy 901 TATGCTTTAGGTGAAGGTGATAAAGTCTTTTCACTGTGGAGGAGGGCTAACTGAT 960  
Db 901 TATGCTTTAGGTGAAGGTGATAAAGTCTTTTCACTGTGGAGGAGGGCTAACTGAT 960  
Qy 961 TGGAAAGCCAGTGAAGACCTTTGGGAAACACATGCTAAATGCTATCCAGGGTSCAAATAT 1020  
Db 961 TGGAAAGCCAGTGAAGACCTTTGGGAAACACATGCTAAATGCTATCCAGGGTSCAAATAT 1020  
Qy 1021 CTGTTAGAACAGAGGACAAAGATATATAACAAATATTCATTTAACTCATTCTGAG 1080  
Db 1021 CTGTTAGAACAGAGGACAAAGATATATAACAAATATTCATTTAACTCATTCTGAG 1080  
Qy 1081 GAGTCTCTGGTAAGAACTACTGAGAAAAACACCATCACTAAGTGAAGAAATTTGATGATACC 1140  
Db 1081 GAGTCTCTGGTAAGAACTACTGAGAAAAACACCATCACTAAGTGAAGAAATTTGATGATACC 1140  
Qy 1141 ATCTTCCAAAATCTTATGGTACAAAGAGCTATACCAATGGGGTTCAGTTTCAAGGACATT 1200  
Db 1141 ATCTTCCAAAATCTTATGGTACAAAGAGCTATACCAATGGGGTTCAGTTTCAAGGACATT 1200  
Qy 1201 AAGAAATTAATGAGGAAAAATTCAGATATCTGGAGCAACTATAAATCATTCTGAGGTT 1260  
Db 1201 AAGAAATTAATGAGGAAAAATTCAGATATCTGGAGCAACTATAAATCATTCTGAGGTT 1260  
Qy 1261 CTGTTGTCAGATCTAGTGAATGCTCAGAAAGACAGTATGCAAGATGAGTCAAGTCAAGCT 1320  
Db 1261 CTGTTGTCAGATCTAGTGAATGCTCAGAAAGACAGTATGCAAGATGAGTCAAGTCAAGCT 1320  
Qy 1321 TCATTACAGAAAGAGATAGTACTCAAGAGCAGCTTAAGCGCCTGCAAGAGGAGAGCTT 1380  
Db 1321 TCATTACAGAAAGAGATAGTACTCAAGAGCAGCTTAAGCGCCTGCAAGAGGAGAGCTT 1380  
Qy 1381 TGCAAAATCTGTATGGATAGAAATATTTGCTATCGTTTTTTTGTTCCTTGTGGACATCTAGTC 1440  
Db 1381 TGCAAAATCTGTATGGATAGAAATATTTGCTATCGTTTTTTTGTTCCTTGTGGACATCTAGTC 1440  
Qy 1441 ACTTGTAAACAAATGCTGAGAGCAGTTGACAAAGTGTCCCATGTGCTACACAGCTCAAT 1500  
Db 1441 ACTTGTAAACAAATGCTGAGAGCAGTTGACAAAGTGTCCCATGTGCTACACAGCTCAAT 1500  
Qy 1501 TTCAGCAAAAAATTTTATGCTTAACTTAATCTATAGTAGGAGCATGTTATGTTGTTCT 1560  
Db 1501 TTCAGCAAAAAATTTTATGCTTAACTTAATCTATAGTAGGAGCATGTTATGTTGTTCT 1560  
Qy 1561 TATTACCCCTGATTGAATGTGTGATGTGAACCTGACCTTTAAGTAATCAGGATTAATCCAT 1620  
Db 1561 TATTACCCCTGATTGAATGTGTGATGTGAACCTGACCTTTAAGTAATCAGGATTAATCCAT 1620  
Qy 1621 TAGCAATTTGCTACCAAGTAGGAAAAAATGTACATGGCAGTGTGTTAGTTGGCAATATA 1680  
Db 1621 TAGCAATTTGCTACCAAGTAGGAAAAAATGTACATGGCAGTGTGTTAGTTGGCAATATA 1680  
Qy 1681 ATCTTTGAATTTCTTGATTTTTCAGGTTATTTAGCTGATTTATCCATTTTTTTTACTGTTA 1740  
Db 1681 ATCTTTGAATTTCTTGATTTTTCAGGTTATTTAGCTGATTTATCCATTTTTTTTACTGTTA 1740

```
QY 1741 TTTAATTGAACCATAGACTAAGAATAAGAAGCATCATACTATAACTGAACAAATCTGT 1800
|||||
Db 1741 TTTAATTGAACCATAGACTAAGAATAAGAAGCATCATACTATAACTGAACAAATGTGT 1800
|||||
QY 1801 ATTCAATAGTATAGTAAATTTCTTAAGTGAAGTGAATTAATCAATCTGGATTTTTTAT 1860
|||||
Db 1801 ATTCAATAGTATAGTAAATTTCTTAAGTGAAGTGAATTAATCAATCTGGATTTTTTAT 1860
|||||
QY 1861 TCTTTTCAGATAGGCTTAACAAATGGAGCTTCTGTATATAAATGTGGAGATTAGAGTTA 1920
|||||
Db 1861 TCTTTTCAGATAGGCTTAACAAATGGAGCTTCTGTATATAAATGTGGAGATTAGAGTTA 1920
|||||
QY 1921 ATCTCCCAATCACATAATTTGTTTGTGTGAAAAAGGAATAAATTTCCATGCTGGTG 1980
|||||
Db 1921 ATCTCCCAATCACATAATTTGTTTGTGTGAAAAAGGAATAAATTTCCATGCTGGTG 1980
|||||
QY 1981 GAAAGATAGAGATTGTTTATAGAGTTGGTTGTGTGTTTAGGATCTGTCCATTTTCT 2040
|||||
Db 1981 GAAAGATAGAGATTGTTTATAGAGTTGGTTGTGTGTTTAGGATCTGTCCATTTTCT 2040
|||||
QY 2041 T 2041
|
Db 2041 T 2041

RESULT 5
US-09-392-580-1
; Sequence 1, Application US/09392580
; Patent No. 6087173
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS EXPRESSION
; FILE REFERENCE: RTS-0072
; CURRENT APPLICATION NUMBER: US/09/392,580
; CURRENT FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (34)..(1527)
US-09-392-580-1

Query Match 38.0%; Score 1990; DB 3; Length 2540;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAAGGTGGACAAGTCCCTATTTTCAAGAGAAGATGACATTTTAAACAGTTTGAAGGATCT 60
|||||
Db 1 GAAAGGTGGACAAGTCCCTATTTTCAAGAGAAGATGACATTTTAAACAGTTTGAAGGATCT 60
|||||
QY 61 AAAAATTTGTACTGCAGACATCAATAGGAAGAAGAATTTCTAGAAGAAGTTTAATAGA 120
|||||
Db 61 AAAAATTTGTACTGCAGACATCAATAGGAAGAAGAATTTCTAGAAGAAGTTTAATAGA 120
|||||
QY 121 TTAATAAATTTTGTCTAATTTTCCAAAGTGTAGTCCCTGTTTCAGCATCAACACTGGCACGA 180
|||||
Db 121 TTAATAAATTTTGTCTAATTTTCCAAAGTGTAGTCCCTGTTTCAGCATCAACACTGGCACGA 180
|||||
QY 181 GCAGGTTTCTTTATCTGTGTGAAGGAGATACCGTGGGTGCTTTTATAGTGTCTATGAGCT 240
|||||
Db 181 GCAGGTTTCTTTATCTGTGTGAAGGAGATACCGTGGGTGCTTTTATAGTGTCTATGAGCT 240
|||||
QY 241 GTAGATAGATGGCAATATGGAGACTCAGCAGTTGGGAAGACACAGGAAGATATCCCAAT 300
|||||
Db 241 GTAGATAGATGGCAATATGGAGACTCAGCAGTTGGGAAGACACAGGAAGATATCCCAAT 300
|||||
QY 301 TGCAGATTTATCAACGGCTTTTATCTTGAAATAGTGCCACGAGCTACAAATTTCTGGT 360
|||||
```

```
Db 301 TGCAGATTTATCAACGGCTTTTATCTTGAAATAGTGCCACGAGCTACAAAATTTCTGGT 360
|||||
QY 361 ATCCAGAAATGGTCAGTACAAAGTTGAAACTATCTGGGAAGCAGAGATCAATTTGCGCTTA 420
|||||
Db 361 ATCCAGAAATGGTCAGTACAAAGTTGAAACTATCTGGGAAGCAGAGATCAATTTGCGCTTA 420
|||||
QY 421 GACAGGCCATCTCTGAGACACATGCAGACTATCTTTTGTAGAACTGGGAGGTTGTAGATATA 480
|||||
Db 421 GACAGGCCATCTCTGAGACACATGCAGACTATCTTTTGTAGAACTGGGAGGTTGTAGATATA 480
|||||
QY 481 TCAGACACCATATACCCGGAGGAACCTGCCATGTATAGTGAAGAAGCTAGATTAAAGTCC 540
|||||
Db 481 TCAGACACCATATACCCGGAGGAACCTGCCATGTATAGTGAAGAAGCTAGATTAAAGTCC 540
|||||
QY 541 TTTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTGGTGAATC 600
|||||
Db 541 TTTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTGGTGAATC 600
|||||
QY 601 TACTACACAGTATTTGGTGACCAAGTGCAGTGTCTTTTGTGTGGTGGAAACTGAAAAAT* 660
|||||
Db 601 TACTACACAGTATTTGGTGACCAAGTGCAGTGTCTTTTGTGTGGTGGAAACTGAAAAAT 660
|||||
QY 661 TGGGAACCTTGTGATCGTGCCTGGTCAGAACACAGGCGACACTTTCCTAATTTGCTTTT 720
|||||
Db 661 TGGGAACCTTGTGATCGTGCCTGGTCAGAACACAGGCGACACTTTCCTAATTTGCTTTT 720
|||||
QY 721 GTTTTGGCCGGAATCTTAATATTCGAAGTGAATCTGATGCTGTGAGTTCTGATAGAAAT 780
|||||
Db 721 GTTTTGGCCGGAATCTTAATATTCGAAGTGAATCTGATGCTGTGAGTTCTGATAGAAAT 780
|||||
QY 781 TTCCCAAAATTCACAAATCTTCCAAAGAAATCCATCCATGGCAGATTATGAAGCACGGATC 840
|||||
Db 781 TTCCCAAAATTCACAAATCTTCCAAAGAAATCCATCCATGGCAGATTATGAAGCACGGATC 840
|||||
QY 841 TTTTACTTTTGGGACATGGATATATCTCAGTTTAAACAAGGAGCAGCTTGCAGAGCTGGATTT 900
|||||
Db 841 TTTTACTTTTGGGACATGGATATATCTCAGTTTAAACAAGGAGCAGCTTGCAGAGCTGGATTT 900
|||||
QY 901 TATGCTTTAGTGAAGTGAATTAAGTAAAGTCTTTTCACTGTGGAGGCGCTTAACATGAT 960
|||||
Db 901 TATGCTTTAGTGAAGTGAATTAAGTAAAGTCTTTTCACTGTGGAGGCGCTTAACATGAT 960
|||||
QY 961 TGGAAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGTTGCAAAATAT 1020
|||||
Db 961 TGGAAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGTTGCAAAATAT 1020
|||||
QY 1021 CTGTTAGACAGAAAGGACAAAGATATATAAACAATATTCATTTAATCTCACTTTGAG 1080
|||||
Db 1021 CTGTTAGACAGAAAGGACAAAGATATATAAACAATATTCATTTAATCTCACTTTGAG 1080
|||||
QY 1081 GAGTGTCTGTAAGAATCTAGAGAAACACCATCACTAACTAGAGAAATGTATGATACC 1140
|||||
Db 1081 GAGTGTCTGTAAGAATCTAGAGAAACACCATCACTAACTAGAGAAATGTATGATACC 1140
|||||
QY 1141 ATCTTCCAAAATCCTATGGTACAAAGAGCTATACGAATGGGTTTCAGTTTCAAGGACATT 1200
|||||
Db 1141 ATCTTCCAAAATCCTATGGTACAAAGAGCTATACGAATGGGTTTCAGTTTCAAGGACATT 1200
|||||
QY 1201 AAGAAATTAATGGAGGAAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTGAGGTT 1260
|||||
Db 1201 AAGAAATTAATGGAGGAAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTGAGGTT 1260
|||||
QY 1261 CTGGTTGCAGATCTAGTGAATGCTCAGAAAGACAGATATGCAAGATAGTCAAGTCAAGT 1320
|||||
Db 1261 CTGGTTGCAGATCTAGTGAATGCTCAGAAAGACAGATATGCAAGATAGTCAAGTCAAGT 1320
|||||
QY 1321 TCATTACAGAAAGAGATTAGTACTGAGAGCAGCTAGGCGCCTGCAAGAGGAGAAAGCTT 1380
|||||
Db 1321 TCATTACAGAAAGAGATTAGTACTGAGAGCAGCTAGGCGCCTGCAAGAGGAGAAAGCTT 1380
|||||
QY 1381 TGCAAAATCTGTATGGATAGAAATATTCCTATGCTTTTGTCTTGTGACATCTAGTCT 1440
|||||
```



```
Db 1381 TGC AAAATCTGTATGATAGAAAATATTGCTATCGTGTATCGTTTTTGTCTCTTGTGGACATCTAGTC 1440
Qy 1441 ACTTGTAAACAATGCTGCTGAAGCAGTTGACAAAGTGTCCTCATGTCCTACACAGTCATTACT 1500
Db 1441 ACTTGTAAACAATGCTGCTGAAGCAGTTGACAAAGTGTCCTCATGTCCTACACAGTCATTACT 1500
Qy 1501 TTCAAGCAAAAATTTTATGCTCTTAATCTAACTACTATAGTAGGCATGTTATGTTGTTCT 1560
Db 1501 TTCAAGCAAAAATTTTATGCTCTTAATCTAACTACTATAGTAGGCATGTTATGTTGTTCT 1560
Qy 1561 TATTACCCGTGAATGAATGCTGATGCTGAACATGACTTTAAAGTAATCAGAGATTGAATTCAT 1620
Db 1561 TATTACCCGTGAATGAATGCTGATGCTGAACATGACTTTAAAGTAATCAGAGATTGAATTCAT 1620
Qy 1621 TAGCATTTGCTACCAAGTAGGAAAAAATGATACATGCGAGTGTTTAGTGGCAATATA 1680
Db 1621 TAGCATTTGCTACCAAGTAGGAAAAAATGATACATGCGAGTGTTTAGTGGCAATATA 1680
Qy 1681 ATCTTTGAAATTTCTTGATTTTTTCAGGGTATTAGCTGTATTATCCATTTTTTTTACTGTTA 1740
Db 1681 ATCTTTGAAATTTCTTGATTTTTTCAGGGTATTAGCTGTATTATCCATTTTTTTTACTGTTA 1740
Qy 1741 TTTAATTGAACCAATAGACTAAGAAATAGAAGCATCATACTATAACTGAACACAATGTGT 1800
Db 1741 TTTAATTGAACCAATAGACTAAGAAATAGAAGCATCATACTATAACTGAACACAATGTGT 1800
Qy 1801 ATTCATAGTACTGATTAAATTTCTAAGTCTAAGTGAATTAATCAATCTGGATTTTTTAT 1860
Db 1801 ATTCATAGTACTGATTAAATTTCTAAGTCTAAGTGAATTAATCAATCTGGATTTTTTAT 1860
Qy 1861 TCTTTTCAGATAGGCTTAAACAAATGGAGCTTTCCTGTATATATAAATGTGGAGATTAGAGTTA 1920
Db 1861 TCTTTTCAGATAGGCTTAAACAAATGGAGCTTTCCTGTATATAAATGTGGAGATTAGAGTTA 1920
Qy 1921 ATCTCCCCAATCACAATATTTGTTGTGTGAAAAAGGAATAAATGTTCCATGCTGGTG 1980
Db 1921 ATCTCCCCAATCACAATATTTGTTGTGTGAAAAAGGAATAAATGTTCCATGCTGGTG 1980
Qy 1981 GAAAGATAGAGATGTTTTTAGAGTTGGTTGTTGTTTGGATTTCTGTCCTGCTCCATTTTCT 2040
Db 1981 GAAAGATAGAGATGTTTTTAGAGTTGGTTGTTGTTTGGATTTCTGTCCTGCTCCATTTTCT 2040
Qy 2041 T 2041
Db 2041 T 2041

RESULT 6
US-09-239-867-3
; Sequence 3, Application US/09239867
; Patent No. 6331412
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; FILE OF INVENTION: MALE FERTILITY
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/09/239,867
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/073,001
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1588
; TYPE: DNA
; ORGANISM: Homo sapiens
us-09-239-867-3

Query Match 30.4%; Score 1588; DB 4; Length 1588;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1588; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAAAGGTGGACAAGTCCTATTTTCAAGAGAAGATGACTTTTAAACAGTTTTTGAAGGATCT 60
```

```
Db 1 GAAAAGGTGGACAAGTCCTATTTTCAAGAGAAGATGACTTTTAAACAGTTTTTGAAGGATCT 60
Qy 61 AAAACTTGTGTACTCTGACGACATCAATAAGGAAGAAGAAATTTGTAGAGAGTTTAAATAGA 120
Db 61 AAAACTTGTGTACTCTGACGACATCAATAAGGAAGAAGAAATTTGTAGAGAGTTTAAATAGA 120
Qy 121 TTA AAAA ACTTTTGTCTAAATTTTCCAAAGTGTAGTCTCTGTTTCAGCATCAACACTGGCAGGA 180
Db 121 TTA AAAA ACTTTTGTCTAAATTTTCCAAAGTGTAGTCTCTGTTTCAGCATCAACACTGGCAGGA 180
Qy 181 GCAGGGTTCCTTTATCTGTTGAAGGAGATACCGTTCGGGTGCTTTAGTGTGCATGCGAGCT 240
Db 181 GCAGGGTTCCTTTATCTGTTGAAGGAGATACCGTTCGGGTGCTTTAGTGTGCATGCGAGCT 240
Qy 241 GTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAAGACACAGAGAAAGTATCCCCAAT 300
Db 241 GTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAAGACACAGAGAAAGTATCCCCAAT 300
Qy 301 TGCAGATTTATCAACGGCTTTTATCTTTGAAAATAGTGCACGCGAGTCTACAAAATCTCGT 360
Db 301 TGCAGATTTATCAACGGCTTTTATCTTTGAAAATAGTGCACGCGAGTCTACAAAATCTCGT 360
Qy 361 ATCCAGAATGTCAGTACAAAAGTTGAAAACCTATCTGGAAGACAGAGATCATTTTGCCTTTA 420
Db 361 ATCCAGAATGTCAGTACAAAAGTTGAAAACCTATCTGGAAGACAGAGATCATTTTGCCTTTA 420
Qy 421 GACAGGCCATCTGAGACACATGCAGACTATCTTTTGAGAACTGGGCGAGTTGTAGATATA 480
Db 421 GACAGGCCATCTGAGACACATGCAGACTATCTTTTGAGAACTGGGCGAGTTGTAGATATA 480
Qy 481 TCAGACACCATATACCCGAGGAACCTGCCATGTATAGTGAAGAGCTAGAGTTAAAGTCC 540
Db 481 TCAGACACCATATACCCGAGGAACCTGCCATGTATAGTGAAGAGCTAGAGTTAAAGTCC 540
Qy 541 TTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGAGAGTTAGCAAGTGTGAGACTC 600
Db 541 TTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGAGAGTTAGCAAGTGTGAGACTC 600
Qy 601 TACTACACAGATATTGTTGACCAAGTCAGTGCTTTTGTGTTGGTGGAAAACTGAAAAAT 660
Db 601 TACTACACAGATATTGTTGACCAAGTCAGTGCTTTTGTGTTGGTGGAAAACTGAAAAAT 660
Qy 661 TGGGAACCTTTGTGATCGTCCGCTGCTCAGACACACAGGCGACACTTTTCCCTAATTTGCTCTTT 720
Db 661 TGGGAACCTTTGTGATCGTCCGCTGCTCAGACACACAGGCGACACTTTTCCCTAATTTGCTCTTT 720
Qy 721 GTTTTGGGCCCGGAATCTTTAATATTTCGAAGTGAATCTGATGCTGTGATAGGAAT 780
Db 721 GTTTTGGGCCCGGAATCTTTAATATTTCGAAGTGAATCTGATGCTGTGATAGGAAT 780
Qy 781 TTCCCAAAATTCACAAATCTTTCCAAAGAAATCCATCCATGGCAGATATTGAAGCAGGATC 840
Db 781 TTCCCAAAATTCACAAATCTTTCCAAAGAAATCCATCCATGGCAGATATTGAAGCAGGATC 840
Qy 841 TTTACTTTTGGGACATGGATATACTCAGTTAAACAGGAGCAGCTTGCAGAGCTGGATTT 900
Db 841 TTTACTTTTGGGACATGGATATACTCAGTTAAACAGGAGCAGCTTGCAGAGCTGGATTT 900
Qy 901 TATGCTTTTAGTGAAGTGATAAAAGTGAAGTGCCTTCACTGTGGAGGAGGCTTAAGTAT 960
Db 901 TATGCTTTTAGTGAAGTGATAAAAGTGAAGTGCCTTCACTGTGGAGGAGGCTTAAGTAT 960
Qy 961 TGGAGGCCAGTGAAGACCTTTGGGAACAACATGCTAAATGGTATCCAGGGTGCAAAATAT 1020
Db 961 TGGAGGCCAGTGAAGACCTTTGGGAACAACATGCTAAATGGTATCCAGGGTGCAAAATAT 1020
Qy 1021 CTGTTTAGAACAGAAGGGACAAGATATATAAACAAATATTTCAATTTAACTCATCTCAGTTGAG 1080
Db 1021 CTGTTTAGAACAGAAGGGACAAGATATATAAACAAATATTTCAATTTAACTCATCTCAGTTGAG 1080
Qy 1081 GAGTGTCTGTTAAGAACTACTGAGAAAAACACCATCACTAACTAGAGAAATTTGATGATACC 1140
Db 1081 GAGTGTCTGTTAAGAACTACTGAGAAAAACACCATCACTAACTAGAGAAATTTGATGATACC 1140
```



```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40328 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-742-185-102

      Query Match      2.0%;      Score 103;      DB 3;      Length 40328;
      Best Local Similarity 100.0%;      Pred. No. 3.3e-31;
      Matches 103;      Conservative 0;      Mismatches 0;      Indels 0;      Gaps

Qy 4955 GCCTGTATATCCAGACACTTTGGGAGGCTGAGCGAGGTGGATCACAGGTCAGGAGATCGA 5014
      |||||
Db 32275 GCCTGTATATCCAGACACTTTGGGAGGCTGAGCGAGGTGGATCACAGGTCAGGAGATCGA 322116

Qy 5015 GACCATCTGCTACACGGTGAACCCGCTCTTACTATAAAA 5057
      |||||
Db 32215 GACCATCTGCTACACGGTGAACCCGCTCTTACTATAAAA 32173

RESULT 8
US-08-742-185-101/c
; Sequence 101, Application US/08742185
; Patent No. 6020476
; GENERAL INFORMATION:
; APPLICANT: Page, David C.
; APPLICANT: Reijo, Renee
; APPLICANT: Saxena, Richa

```

APPLICANT: REEVE, MARY PAT  
TITLE OF INVENTION: DAZ: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA

TITLE OF INVENTION: DA2: A GENE FAMILY ASSOCIATED WITH ACIDOSPERMIA  
 NUMBER OF SEQUENCES: 102  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
 STREET: Two Militia Drive  
 CITY: Lexington  
 STATE: Massachusetts  
 COUNTRY: US  
 ZIP: 02173  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/742,185  
 FILING DATE: 30-OCT-1996  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/690,734  
 FILING DATE: 31-JUL-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/310,429  
 FILING DATE: 22-SEP-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Granahan, Patricia  
 REGISTRATION NUMBER: 32,227  
 REFERENCE/DOCKET NUMBER: WHI94-07A2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 861-6240  
 TELEFAX: (617) 861-9540  
 INFORMATION FOR SEQ ID NO: 101:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 43795 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)



```
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/154 NIHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11298 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; STRAIN: FcRI beta
; US-07-869-933-31

Query Match 1.3%; Score 70; DB 1; Length 11298;
Best Local Similarity 100.0%; Pred. No. 2.4e-18;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4989 GGTGGATCAGGAGTCAGAGATCGAGACCATCTGGCTAAACACGGTGAACCCCGTCTC 5048
|||||
Db 10775 GGTGGATCAGGAGTCAGAGATCGAGACCATCTGGCTAAACACGGTGAACCCCGTCTC 10834

QY 5049 TACTAAAAA 5058
|||||
Db 10835 TACTAAAAA 10844

RESULT 13
US-08-201-879A-2
; Sequence 2, Application US/08201879A
; Patent No. 5807988
; GENERAL INFORMATION:
; APPLICANT: KINET, Jean-Pierre
; APPLICANT: JOUVIN, Marie-Helene
; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
; TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
; TITLE OF INVENTION: IMMUNOGLOBULIN E
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/201,879A
; FILING DATE: 24-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/869,933
; FILING DATE: 16-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/03419
; FILING DATE: 16-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/234/NIHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
```

```
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11298 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; STRAIN: FcRI beta
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(456..511, 1381..1510, 2026..2160, 4475..4531,
; LOCATION: 5079..5237, 5640..5738, 7224..7319)
; US-08-201-879A-2

Query Match 1.3%; Score 70; DB 1; Length 11298;
Best Local Similarity 100.0%; Pred. No. 2.4e-18;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4989 GGTGGATCAGGAGTCAGAGATCGAGACCATCTGGCTAAACACGGTGAACCCCGTCTC 5048
|||||
Db 10775 GGTGGATCAGGAGTCAGAGATCGAGACCATCTGGCTAAACACGGTGAACCCCGTCTC 10834

QY 5049 TACTAAAAA 5058
|||||
Db 10835 TACTAAAAA 10844

RESULT 14
US-09-103-663-31
; Sequence 31, Application US/09103663D
; Patent No. 6171803
; GENERAL INFORMATION:
; APPLICANT: Kinet et al.
; TITLE OF INVENTION: Isolation, characterization, and use of the human beta
; TITLE OF INVENTION: subunit of the high affinity receptor for
; TITLE OF INVENTION: immunoglobulin E.
; FILE REFERENCE: 50490
; CURRENT APPLICATION NUMBER: US/09/103,663D
; CURRENT FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 07/869,933
; EARLIER FILING DATE: 1992-04-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 11298
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-103-663-31

Query Match 1.3%; Score 70; DB 4; Length 11298;
Best Local Similarity 100.0%; Pred. No. 2.4e-18;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4989 GGTGGATCAGGAGTCAGAGATCGAGACCATCTGGCTAAACACGGTGAACCCCGTCTC 5048
|||||
Db 10775 GGTGGATCAGGAGTCAGAGATCGAGACCATCTGGCTAAACACGGTGAACCCCGTCTC 10834

QY 5049 TACTAAAAA 5058
|||||
Db 10835 TACTAAAAA 10844

RESULT 15
US-08-520-373D-4
; Sequence 4, Application US/08520373D
; Patent No. 6451763
; GENERAL INFORMATION:
; APPLICANT: Tombran-Tink, Joyce
; APPLICANT: Steele, Fintan R
; APPLICANT: Chader, Gerald J
; APPLICANT: Becerra, Sofia P
; APPLICANT: Johnson, Lincoln V
```



GenCore version 5.1.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 00:05:56 ; Search time 164 Seconds  
(without alignments)  
11318.521 Million cell updates/sec

Title: US-09-974-592-3  
Perfect score: 5232  
Sequence: 1 gaaagggtggacaagtccta.....tcaaaaaaaaaaaaaaag 5232

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 320260 seqs, 177392727 residues

Word size : 0

Total number of hits satisfying chosen parameters: 640520

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published\_Applications\_NA.\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US05\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/2/pubpna/FCUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5232	100.0	5232	10	US-09-974-592-3
C 2	466	8.9	489	10	Sequence 3, Appl1
C 3	148	2.8	148	10	Sequence 13853, A
4	89	1.7	194	10	Sequence 30419, A
5	85	1.6	53542	10	Sequence 2426, Ap
C 6	78	1.5	302250	10	Sequence 61, Appl
C 7	77	1.5	203654	10	Sequence 154, App
C 8	76	1.5	401	10	Sequence 3, Appl1
C 9	76	1.5	401	10	Sequence 421, App
C 10	74	1.4	19736	12	Sequence 421, App
C 11	73	1.4	1503841	10	Sequence 3, Appl1
C 12	73	1.4	1503841	10	Sequence 1, Appl1
C 13	72	1.4	30420	10	Sequence 1, Appl1
14	71	1.4	362	10	Sequence 2432, Ap
15	70	1.3	281	10	Sequence 7428, Ap
16	69	1.3	226	10	Sequence 643, App
17	69	1.3	292	10	Sequence 1423, Ap
18	69	1.3	292	10	Sequence 1844, Ap
C 19	69	1.3	342	10	Sequence 1847, Ap
					Sequence 8277, Ap

20	1.3	739	10	US-09-764-877-3833	Sequence 3833, Ap
C 21	69	1.3	1400	10	Sequence 295, App
22	69	1.3	1408	10	Sequence 1489, Ap
23	69	1.3	4378	10	Sequence 355, App
C 24	69	1.3	6186	10	Sequence 1075, Ap
C 25	69	1.3	9745	10	Sequence 2259, Ap
C 26	69	1.3	12149	10	Sequence 2258, Ap
C 27	69	1.3	15070	10	Sequence 3979, Ap
C 28	69	1.3	15071	10	Sequence 3978, Ap
C 29	69	1.3	18071	10	Sequence 17, Appl
C 30	69	1.3	18385	10	Sequence 1018, Ap
C 31	69	1.3	22484	10	Sequence 2, Appl1
32	69	1.3	22484	10	Sequence 3341, Ap
C 33	69	1.3	43058	10	Sequence 292, App
C 34	69	1.3	43058	10	Sequence 529, App
C 35	69	1.3	43058	10	Sequence 3950, Ap
C 36	69	1.3	52216	10	Sequence 1, Appl1
C 37	69	1.3	110096	10	Sequence 1542, Ap
C 38	69	1.3	116592	10	Sequence 3, Appl1
C 39	69	1.3	684973	10	Sequence 1, Appl1
40	68	1.3	463	10	Sequence 112, App
41	68	1.3	32195	10	Sequence 611, App
42	68	1.3	32195	10	Sequence 617, App
43	68	1.3	32195	10	Sequence 1605, Ap
C 44	68	1.3	174493	10	Sequence 3, Appl1
C 45	67	1.3	26048	10	Sequence 1556, Ap

ALIGNMENTS

RESULT 1  
US-09-974-592-3  
; Sequence 3, Application US/09974592  
; Patent No. US20020120121A1  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G  
; APPLICANT: Mackenzie, Alexander E  
; APPLICANT: Liston, Peter  
; APPLICANT: Baird, Stephen  
; APPLICANT: Tsang, Benjamin K  
; APPLICANT: Pratt, Christine  
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
; TITLE OF INVENTION: DISEASE  
; FILE REFERENCE: 07891/009004  
; CURRENT APPLICATION NUMBER: US/09/974,592  
; CURRENT FILING DATE: 2001-10-09  
; PRIOR APPLICATION NUMBER: US 09/617,053  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 08/800,929  
; PRIOR FILING DATE: 1997-02-13  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 5232  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: variation  
; LOCATION: 4623  
; OTHER INFORMATION: n can be any nucleotide  
; NAME/KEY: variation  
; LOCATION: 4622  
; OTHER INFORMATION: n can be any nucleotide  
US-09-974-592-3  
Query Match 100.0%; Score 5232; DB 10; Length 5232;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAAAGGTGACAAAGTCCTATTTTCAAGAGAAGATGACTTTTACAGCTTTTGAAGATCT 60  
|||||

Db 1 GAAAGGTGGCAAGCTCCTATTTTCAAGAGAAAGATGACTTTTAAACAGTTTTTGAAGGATCT 60  
Qy 61 AAAATTGTGTACCTGCAGACATCAATTAAGGAAGAATTTGTAGAGAGTTTAAATAGA 120  
Db 61 AAAATTGTGTACCTGCAGACATCAATTAAGGAAGAATTTGTAGAGAGTTTAAATAGA 120  
Qy 121 TTAATAACTTTTGTCTAATTTTCCAAAGTGGTAGTCTCTTTTCAGCATCAACACTGGCAGCA 180  
Db 121 TTAATAACTTTTGTCTAATTTTCCAAAGTGGTAGTCTCTTTTCAGCATCAACACTGGCAGCA 180  
Qy 181 GCAGGGTTCTTTTATCTGTTGAAGGAGATACCGTGGCGGTCTTTTGTGTCAGCT 240  
Db 181 GCAGGGTTCTTTTATCTGTTGAAGGAGATACCGTGGCGGTCTTTTGTGTCAGCT 240  
Qy 241 GTAGATAGTGGCAATATGAGACTCAGCAGTTGGAAGACACAGAGAAAGTATCCCCAAAT 300  
Db 241 GTAGATAGTGGCAATATGAGACTCAGCAGTTGGAAGACACAGAGAAAGTATCCCCAAAT 300  
Qy 301 TGCAGATTTATCAACGGCTTTTATCTTGAATAATAGTGGCAGCAGTCTACAAATTCCTGGT 360  
Db 301 TGCAGATTTATCAACGGCTTTTATCTTGAATAATAGTGGCAGCAGTCTACAAATTCCTGGT 360  
Qy 361 ATCCAGAAATGCTCAGTACAAGTTGAAGACTATCTGGAAGCAGAGATCAATTTGCCCTTA 420  
Db 361 ATCCAGAAATGCTCAGTACAAGTTGAAGACTATCTGGAAGCAGAGATCAATTTGCCCTTA 420  
Qy 421 GACAGGCATCTGAGACACATGACAGATATCTTTTGAGAACTGGCGAGTTGTAGATATA 480  
Db 421 GACAGGCATCTGAGACACATGACAGATATCTTTTGAGAACTGGCGAGTTGTAGATATA 480  
Qy 481 TCAGACACATATACCGAGAGACCCCTGCCATGTATAGTGAAGAAGCTAGATTAAGTCC 540  
Db 481 TCAGACACATATACCGAGAGACCCCTGCCATGTATAGTGAAGAAGCTAGATTAAGTCC 540  
Qy 541 TTTCCAGAACTGGCCAGACTATGCTCACCTACCCCAAGAGAGTTAGCAGTGGTGGACTC 600  
Db 541 TTTCCAGAACTGGCCAGACTATGCTCACCTACCCCAAGAGAGTTAGCAGTGGTGGACTC 600  
Qy 601 TACTACACAGATTTGGTGACAAAGTCAAGTGCCTTTTGTGTTGGTGAAGAACTGAAAT 660  
Db 601 TACTACACAGATTTGGTGACAAAGTCAAGTGCCTTTTGTGTTGGTGAAGAACTGAAAT 660  
Qy 661 TGGAACTTGTGATCGTGGCTGCTGAGACACAGGCGACACTTTTCCATTAATGCTTCTTT 720  
Db 661 TGGAACTTGTGATCGTGGCTGCTGAGACACAGGCGACACTTTTCCATTAATGCTTCTTT 720  
Qy 721 GTTTTGGCCGGAATCTTAATATTGGAAGTGAATCTGATGCTGTGAGTCTCTGTAGGAAT 780  
Db 721 GTTTTGGCCGGAATCTTAATATTGGAAGTGAATCTGATGCTGTGAGTCTCTGTAGGAAT 780  
Qy 781 TTCCCAATTCACAAATCTTTCCAAAGAAATCCATCCATGCGAGATTAAGACACGGATC 840  
Db 781 TTCCCAATTCACAAATCTTTCCAAAGAAATCCATCCATGCGAGATTAAGACACGGATC 840  
Qy 841 TTTACTTTTGGACATGGATATCTCAGTTTAAAGAGAGAGAGCTTGAAGAGCTGGATTT 900  
Db 841 TTTACTTTTGGACATGGATATCTCAGTTTAAAGAGAGAGAGCTTGAAGAGCTGGATTT 900  
Qy 901 TATCCTTTAGTGAAGTGAATAAGTAAAGTGTCTTCACTGTGGAGGAGCTTAACATGAT 960  
Db 901 TATCCTTTAGTGAAGTGAATAAGTAAAGTGTCTTCACTGTGGAGGAGCTTAACATGAT 960  
Qy 961 TGGAAAGCCAGTGAAGACCTTTGGGAACAACATGCTAAATGGTATCCAGGCTGCAAAATAT 1020  
Db 961 TGGAAAGCCAGTGAAGACCTTTGGGAACAACATGCTAAATGGTATCCAGGCTGCAAAATAT 1020  
Qy 1021 CTGTTTGAACAGAGGACAGAAATATATAAACAATATTCATTTAACTCACTTCTGAG 1080  
Db 1021 CTGTTTGAACAGAGGACAGAAATATATAAACAATATTCATTTAACTCACTTCTGAG 1080  
Qy 1081 GAGTGTCTGTTGAAGTCTTACTGGAAGAACACCTACATCACTAGAGAATTTGATGATACC 1140  
Db 1081 GAGTGTCTGTTGAAGTCTTACTGGAAGAACACCTACATCACTAGAGAATTTGATGATACC 1140

Qy 1141 ATCTTCCAAATCCTATGGTACAAAGAGCTATACGAATGGGGTTTCAAGGACATTT 1200  
Db 1141 ATCTTCCAAATCCTATGGTACAAAGAGCTATACGAATGGGGTTTCAAGGACATTT 1200  
Qy 1201 AAGAAATTAATGGAGGAAAAATTCAGATATCTGGGAGCACTATAATCACTTTGAGGTT 1260  
Db 1201 AAGAAATTAATGGAGGAAAAATTCAGATATCTGGGAGCACTATAATCACTTTGAGGTT 1260  
Qy 1261 CTGGTTCCAGATCTAGTGAATGCTCAGAAAGACAGTATGCAAGATGAGTCAAGTCAGACT 1320  
Db 1261 CTGGTTCCAGATCTAGTGAATGCTCAGAAAGACAGTATGCAAGATGAGTCAAGTCAGACT 1320  
Qy 1321 TCATTTACAGAAAGAGATTAGTACTGAAAGAGCAGCTAAGGCGCTTGAAGAGGAGAAAGCTT 1380  
Db 1321 TCATTTACAGAAAGAGATTAGTACTGAAAGAGCAGCTAAGGCGCTTGAAGAGGAGAAAGCTT 1380  
Qy 1381 TGCAAAATCTGTATGGATAGAAATATTTGCTATCGTTTGTCTTCTTGGACATCTAGTC 1440  
Db 1381 TGCAAAATCTGTATGGATAGAAATATTTGCTATCGTTTGTCTTCTTGGACATCTAGTC 1440  
Qy 1441 ACTTGTAAACAATCTGCTGAAGCAGTTTGACAAGTGTCCCATGTCTACACAGTCAATTACT 1500  
Db 1441 ACTTGTAAACAATCTGCTGAAGCAGTTTGACAAGTGTCCCATGTCTACACAGTCAATTACT 1500  
Qy 1501 TTCAAGCAAAAAATTTTATGCTTAATCTAACTCTATAGTAGGCATGTTATGTTGTTCT 1560  
Db 1501 TTCAAGCAAAAAATTTTATGCTTAATCTAACTCTATAGTAGGCATGTTATGTTGTTCT 1560  
Qy 1561 TATTACCCCTGATTGAATGTGTGATGTGAAGTCACTTAAAGTAATCAGGATTTGAATTCAT 1620  
Db 1561 TATTACCCCTGATTGAATGTGTGATGTGAAGTCACTTAAAGTAATCAGGATTTGAATTCAT 1620  
Qy 1621 TAGCATTTGCTACCAAGTAGGAAAAAATCTACATGSCAGTGTGTTAGTTGGCAATATA 1680  
Db 1621 TAGCATTTGCTACCAAGTAGGAAAAAATCTACATGSCAGTGTGTTAGTTGGCAATATA 1680  
Qy 1681 ATCTTTGAATTTCTTGATTTTTCAGGGTATTAGCTGTTATATCCATTTTCTACTGTTA 1740  
Db 1681 ATCTTTGAATTTCTTGATTTTTCAGGGTATTAGCTGTTATATCCATTTTCTACTGTTA 1740  
Qy 1741 TTTAATTTGAACCAATAGACTAAGAAATGAAGAGCATCATATACTTAACCTGAACACAAATGTT 1800  
Db 1741 TTTAATTTGAACCAATAGACTAAGAAATGAAGAGCATCATATACTTAACCTGAACACAAATGTT 1800  
Qy 1801 ATTCATAGTATACCTGATTTAAATTTCTAAGTGAAGTAAATTAATCACTGGAATTTTAT 1860  
Db 1801 ATTCATAGTATACCTGATTTAAATTTCTAAGTGAAGTAAATTAATCACTGGAATTTTAT 1860  
Qy 1861 TCTTTTCAGATAGCTTTAACAATGGAGCTTTCGTATATAAATGTGGAGATTAGAGTTA 1920  
Db 1861 TCTTTTCAGATAGCTTTAACAATGGAGCTTTCGTATATAAATGTGGAGATTAGAGTTA 1920  
Qy 1921 ATCTCCCAATCAGATTAATTTGTTGTCGCAAAAGAAATTAATTTCCATCTCTGCTG 1980  
Db 1921 ATCTCCCAATCAGATTAATTTGTTGTCGCAAAAGAAATTAATTTCCATCTCTGCTG 1980  
Qy 1981 GAAAGATAGAGATTTGTTTAGAGGTTGTTGTTGTTTAGGATTTCTGCTCAATTTCT 2040  
Db 1981 GAAAGATAGAGATTTGTTTAGAGGTTGTTGTTGTTTAGGATTTCTGCTCAATTTCT 2040  
Qy 2041 TTTAAAGTTTAAACAGCTACTTGTGCGAATTAATTTTTTAAAGTGAATTTGCCATTTTG 2100  
Db 2041 TTTAAAGTTTAAACAGCTACTTGTGCGAATTAATTTTTTAAAGTGAATTTGCCATTTTG 2100  
Qy 2101 AAAGCGTATTAAATGATAGAAATCTATCGAGCCCAACATGACTGACATGGAAGATGTCA 2160  
Db 2101 AAAGCGTATTAAATGATAGAAATCTATCGAGCCCAACATGACTGACATGGAAGATGTCA 2160  
Qy 2161 AAGATATGTTAAAGTGAAGTAAAAATGCAAGTGGCAAAACACTATGATAGTCTGAGCCAGATCA 2220  
Db 2161 AAGATATGTTAAAGTGAAGTAAAAATGCAAGTGGCAAAACACTATGATAGTCTGAGCCAGATCA 2220





Db 4381 CAAGTCACCACTTATTTTACATTTTACTCATGCAAGAAATTCAGTAGCTTTTGGCAATAGT 4440  
Qy 4441 ACTTATCTTTTATTTGTAATAATTTAGTCTGCTGATCAAAAAGCAATTTGCTTAAATTTTGGAG 4500  
Db 4441 ACTTATCTTTTATTTGTAATAATTTAGTCTGCTGATCAAAAAGCAATTTGCTTAAATTTTGGAG 4500  
Qy 4501 AACTGGTTTTAGCAATTTACAACTAAATTCAGTTAAATTAATTAAGAGCTTTATATTGGCC 4560  
Db 4501 AACTGGTTTTAGCAATTTACAACTAAATTCAGTTAAATTAATTAAGAGCTTTATATTGGCC 4560  
Qy 4561 TTTCCTGCTACATTTGTTTTTTTCCCTGTCCTTTGATTTACGGGCTAAAGTAGGGTAAG 4620  
Db 4561 TTTCCTGCTACATTTGTTTTTTTCCCTGTCCTTTGATTTACGGGCTAAAGTAGGGTAAG 4620  
Qy 4621 ANNGGGTGTAGTGTAT 4680  
Db 4621 ANNGGGTGTAGTGTAT 4680  
Qy 4681 TTTTGTGTTAT 4740  
Db 4681 TTTTGTGTTAT 4740  
Qy 4741 AAAATTTGTATTTTGAACAT 4800  
Db 4741 AAAATTTGTATTTTGAACAT 4800  
Qy 4801 TACCTTTAAACCCGAATCATTTGTTTTATTTTCCCTGATTTACACAGGCTTTGAAATGGGAAA 4860  
Db 4801 TACCTTTAAACCCGAATCATTTGTTTTATTTTCCCTGATTTACACAGGCTTTGAAATGGGAAA 4860  
Qy 4861 GGGCTGTAT 4920  
Db 4861 GGGCTGTAT 4920  
Qy 4921 ATGAATAAAT 4980  
Db 4921 ATGAATAAAT 4980  
Qy 4981 CTGAGGAGGTGGATACGAGGTCAGGAGATCGAGAGATCGAGACCATCTGGCTTAACACGGTGAAC 5040  
Db 4981 CTGAGGAGGTGGATACGAGGTCAGGAGATCGAGAGATCGAGACCATCTGGCTTAACACGGTGAAC 5040  
Qy 5041 CCCGTCTCTACTATAAACAAGAAATTTAGCGGGCGTGTGGGGCGGCGCTGTAGTCCCA 5100  
Db 5041 CCCGTCTCTACTATAAACAAGAAATTTAGCGGGCGTGTGGGGCGGCGCTGTAGTCCCA 5100  
Qy 5101 GCTACTCGGGAGGCTGAGGAGGAGATGTGTGAACCCGAGGAGGAGCTTTCAGTGA 5160  
Db 5101 GCTACTCGGGAGGCTGAGGAGGAGATGTGTGAACCCGAGGAGGAGCTTTCAGTGA 5160  
Qy 5161 GCCGAGATCTCGCCACTGCACTCCAGGCTGGGCAACAGAGCAAGACTCTGTCTCAAAAAA 5220  
Db 5161 GCCGAGATCTCGCCACTGCACTCCAGGCTGGGCAACAGAGCAAGACTCTGTCTCAAAAAA 5220  
Qy 5221 AAAAAAAG 5232  
Db 5221 AAAAAAAG 5232

RESULT 2  
US-09-864-761-13853/c  
; Sequence 13853, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
; FILE REFERENCE: Aeomica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 13853  
; LENGTH: 489  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AL022156.1  
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.1  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.1  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1  
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.8  
; US-09-864-761-13853

Query Match 8.9%; Score 466; DB 10; Length 489;  
Best Local Similarity 100.0%; Pred. No. 1.5e-150;  
Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1332 AGAGATTAGTACTGAAGAGCAGCTAAGCGCTGCACAGAGAGAGAGCTTTGCAAAATCTG 1391  
Db 466 AGAGATTAGTACTGAAGAGCAGCTAAGCGCTGCACAGAGAGAGAGCTTTGCAAAATCTG 407  
Qy 1392 TATGGATAGAAATATCTCTATCGTTTTTGTTCCTTGTGGACATCTAGTCACTTCTGTAACA 1451  
Db 406 TATGGATAGAAATATCTCTATCGTTTTTGTTCCTTGTGGACATCTAGTCACTTCTGTAACA 347  
Qy 1452 ATGTGCTGAAGCAGTGTGACAAAGTGTCCCATGTGTACACAGTCAATTAATTTCAAGCAAAA 1511  
Db 346 ATGTGCTGAAGCAGTGTGACAAAGTGTCCCATGTGTACACAGTCAATTAATTTCAAGCAAAA 287  
Qy 1512 AATTTTTATGCTCTTAATCTAACTATAGTAGGCAATGTATGTTGTTCTTATTAACCTGA 1571  
Db 286 AATTTTTATGCTCTTAATCTAACTATAGTAGGCAATGTATGTTGTTCTTATTAACCTGA 227  
Qy 1572 TTGAATGTGTGATGTGAACGTGACCTTTAAGTAATCAGGATTTGAATTCATTAAGCATTTGCT 1631  
Db 226 TTGAATGTGTGATGTGAACGTGACCTTTAAGTAATCAGGATTTGAATTCATTAAGCATTTGCT 167

Qy	1632	ACCAAGTAGGAAAAAAATGTACATGGCAGTGTTTTACTGTGCGAATAATAATCTTTGAATT	1691
Db	166	ACCAAGTAGSAAAAAAATGTACATGGCAGTGTTTTACTGTGCGAATAATAATCTTTGAATT	107
Qy	1592	TCATTGATTTTTTCAGGATATAGCTGTATATATCCATTTTTTTTTTACGTATTATTAATGAAA	1751
Db	106	TCATTGATTTTTTCAGGATATAGCTGTATATATCCATTTTTTTTTTACTGTTATTATTAATGAAA	47
Qy	1752	CCATAGACTAAGAATAAAGAAGCATCATACTATACTGAACACAATG	1797
Db	46	CCATAGACTAAGAATAAAGAAGCATCATACTATACTGAACACAATG	1

```

RESULT 3
US-09-864-761-30419/c
; Sequence 30419, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 30419
; LENGTH: 148
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL022156.1
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.1

```

```

; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.8
; OTHER INFORMATION: HIT HIT: U32974.1, EVALUE 4.00e-78
; OTHER INFORMATION: SWISSPROT HIT: P98170, EVALUE 7.00e-17
; OTHER INFORMATION: EST_HUMAN HIT: AI628066.1, EVALUE 5.00e-68
US-09-864-761-30419

Query Match          2.8%; Score 148; DB 10; Length 148;
Best Local Similarity 100.0%; Pred. No. 7.4e-42;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1334 AGATTAGTACTGAAGACGACGCTAAGGCCCTGCAAGAGAGAGAGCTTTGC AAAATCTGTA 1393
DB 148 AGATTAGTACTGAAGACGACGCTAAGGCCCTGCAAGAGAGAGAGCTTTGC AAAATCTGTA 89
QY 1394 TGGATAGAAATATTGCTATCTGTTTGTTCCTTGTGGACATCTAGTCACTTGTAAACAAT 1453
DB 88 TGGATAGAAATATTGCTATCTGTTTGTTCCTTGTGGACATCTAGTCACTTGTAAACAAT 29
QY 1454 GTGCTGAAGCAGTTGCACAAGTGTCCCAT 1481
DB 28 GTGCTGAAGCAGTTGCACAAGTGTCCCAT 1

RESULT 4
US-09-764-877-2426
; Sequence 2426, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764.877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2426
; LENGTH: 194
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-2426

Query Match          1.7%; Score 89; DB 10; Length 194;
Best Local Similarity 100.0%; Pred. No. 1e-21;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4955 GCCTGTAATCCAGCACCTTTGGAGGCTTGAGCGAGGTGATCACAGGTTCAGGAGATCGA 5014
DB 18 GCCTGTAATCCAGCACCTTTGGAGGCTTGAGCGAGGTGATCACAGGTTCAGGAGATCGA 77
QY 5015 GACCATCTGCTACACGGTGAAACCCC 5043
DB 78 GACCATCTGCTACACGGTGAAACCCC 106

RESULT 5
US-09-801-574-61
; Sequence 61, Application US/09801574
; Patent No. US20020081592A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Peijiang Jeremy
; APPLICANT: Page, David C.
; TITLE OF INVENTION: Reproduction-Specific Genes
; FILE REFERENCE: 0399.2007-002
; CURRENT APPLICATION NUMBER: US/09/801.574
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: 60/187,518
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: 60/261,557
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 90

```

[illegible]

```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-795-686-421

Query Match      1.5%; Score 76; DB 10; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.5e-17;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4983 GAGCAGGTGGATCACGAGGTCAGGATCGAGACCATCCCTGGCTAACACGCGTGAACCC 5042
|||||
Db 129 GAGCAGGTGGATCACGAGGTCAGGATCGAGACCATCCCTGGCTAACACGCGTGAACCC 70
|||||

QY 5043 CGTCTCTACTAAAAA 5058
|||||
Db 69 CGTCTCTACTAAAAA 54
|||||

RESULT 10
US-10-014-502-3
; Sequence 3, Application US/10014502
; Patent No. US20020137184A1
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: CU001058DIV
; CURRENT APPLICATION NUMBER: US/10/014,502
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 09/740,035
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 19736
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-014-502-3

Query Match      1.4%; Score 74; DB 12; Length 19736;
Best Local Similarity 100.0%; Pred. No. 7.3e-17;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5066 TTAGCCGGCGGTGGTGGCGGCGCTGTAGTCCAGCTACTCGGGAGGCTGAGGCAGGAG 5125
|||||
Db 13951 TTAGCCGGCGGTGGTGGCGGCGCTGTAGTCCAGCTACTCGGGAGGCTGAGGCAGGAG 14010
|||||

QY 5126 AATGGTGTGAACCC 5139
|||||
Db 14011 AATGGTGTGAACCC 14024
|||||

RESULT 11
US-09-795-686-1/c
; Sequence 1, Application US/09795686
; Patent No. US2002004557A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinthorsdottir, Valgerdur
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2004-001
; CURRENT APPLICATION NUMBER: US/09/795,686
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/515,716
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1503841
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: r=g or a
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: y=t/u or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: m=a or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: k=g or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: s=g or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: w=a or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: b=g or c or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: d=a or g or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: h=a or c or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: v=a or g or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: n=a or g or c or t/u
US-09-795-686-1

Query Match      1.4%; Score 73; DB 10; Length 1503841;
Best Local Similarity 100.0%; Pred. No. 9.1e-17;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5089 CCTGTAGTCCCGAGCTACTCGGGAGGCTGAGGCAGGAGATGGTGTGAACCCGGGAGGCAG 5148
|||||
Db 1501676 CCTGTAGTCCCGAGCTACTCGGGAGGCTGAGGCAGGAGATGGTGTGAACCCGGGAGGCAG 1501617
|||||

QY 5149 AGCTTGCAGTGAG 5161
|||||
Db 1501616 AGCTTGCAGTGAG 1501604
|||||

RESULT 12
US-09-795-686-1/c
; Sequence 1, Application US/09795686
; Patent No. US20020094954A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinthorsdottir, Valgerdur
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2005-001
; CURRENT APPLICATION NUMBER: US/09/795,686
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,715
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1503841
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: r=g or a
; NAME/KEY: misc_feature
```

```
; LOCATION: (1)...(1531)
; OTHER INFORMATION: y=t/u or c
; NAME/KEY: misc.feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: m-a or c
; NAME/KEY: misc.feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: k-g or t/u
; NAME/KEY: misc.feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: s-g or c
; NAME/KEY: misc.feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: w-a or t/u
; NAME/KEY: misc.feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: b-g or c or t/u
; NAME/KEY: misc.feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: d-a or g or t/u
; NAME/KEY: misc.feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: h-a or c or t/u
; NAME/KEY: misc.feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: v-a or g or c
; NAME/KEY: misc.feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: n-a or g or c or t/u
US-09-795-686-1

Query Match      1.4%; Score 73; DB 10; Length 1503841;
Best Local Similarity 100.0%; Pred. No. 9.1e-17;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5089 CCTGTAGTCCAGCTCTCGGAGGCTGAGCGAGGAGATGTTGAACCCGGGAGGCAG 5148
|||||
Db 1501676 CCTGTAGTCCAGCTCTCGGAGGCTGAGCGAGGAGATGTTGAACCCGGGAGGCAG 1501617

QY 5149 AGCTTGCACTGAG 5161
|||||
Db 1501616 AGCTTGCACTGAG 1501604

RESULT 13
US-09-764-877-2432
; Sequence 2432, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2432
; LENGTH: 30420
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-2432

Query Match      1.4%; Score 72; DB 10; Length 30420;
Best Local Similarity 100.0%; Pred. No. 3.3e-16;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5075 CTGGTGGCGGGCGCTGTAGTCCAGCTACTCGGAGGCTGAGCGAGGAGATGGTGTG 5134
|||||
Db 3832 CTGGTGGCGGGCGCTGTAGTCCAGCTACTCGGAGGCTGAGCGAGGAGATGGTGTG 3891

QY 5135 AACCCGGGAGGC 5146
|||||
```

```
Db 3892 AACCCGGGAGGC 3903

RESULT 14
US-09-867-701-7428
; Sequence 7428, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Robert
; APPLICANT: Aglate, Paul A.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7428
; LENGTH: 362
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-7428

Query Match      1.4%; Score 71; DB 10; Length 362;
Best Local Similarity 100.0%; Pred. No. 1.3e-15;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4956 CCTGTAATCCAGCAGCTTTGGAGGCTGAGCGAGGTGGATCAGAGGTGCGAG 5015
|||||
Db 91 CCTGTAATCCAGCAGCAGCTTTGGAGGCTGAGCGAGGTGGATCAGAGGTGCGAG 150

QY 5016 ACCATCCTGGC 5026
|||||
Db 151 ACCATCCTGGC 161

RESULT 15
US-09-764-887-643
; Sequence 643, Application US/09764887
; Patent No. US20020042096A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA113
; CURRENT APPLICATION NUMBER: US/09/764,887
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 658
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 643
; LENGTH: 281
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-887-643

Query Match      1.3%; Score 70; DB 10; Length 281;
Best Local Similarity 100.0%; Pred. No. 3e-15;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5100 AGCTACTCGGAGGCTGAGCGAGGAGATGGTGTGAACCCGGGAGGAGCTTGCAGTG 5159
|||||
Db 148 AGCTACTCGGAGGCTGAGCGAGGAGATGGTGTGAACCCGGGAGGAGCTTGCAGTG 207

QY 5160 AGCCGAGATC 5169
|||||
Db 208 AGCCGAGATC 217

Search completed: November 10, 2002, 04:53:38
Job time : 1443 secs
```

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 9, 2002, 19:48:11 ; Search time 10463 Seconds  
(without alignments)  
12572.445 Million cell updates/sec

Title: US-09-974-592-3  
Perfect score: 5232  
Sequence: 1 gaaaggtgacaaagtctcta.....tcaaaaaaaaaaaaaaaag 5232

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 24791104 seqs, 12571243825 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending\_Patents\_NA\_Main:\*  
1: /cgn2\_6/ptodata/2/pna/PCTUS\_COMB.seq:\*  
2: /cgn2\_6/ptodata/2/pna/US06\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/pna/US07\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/pna/US08\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/pna/US081\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/pna/US082\_COMB.seq:\*  
7: /cgn2\_6/ptodata/2/pna/US083\_COMB.seq:\*  
8: /cgn2\_6/ptodata/2/pna/US084\_COMB.seq:\*  
9: /cgn2\_6/ptodata/2/pna/US085\_COMB.seq:\*  
10: /cgn2\_6/ptodata/2/pna/US086\_COMB.seq:\*  
11: /cgn2\_6/ptodata/2/pna/US087\_COMB.seq:\*  
12: /cgn2\_6/ptodata/2/pna/US088\_COMB.seq:\*  
13: /cgn2\_6/ptodata/2/pna/US089\_COMB.seq:\*  
14: /cgn2\_6/ptodata/2/pna/US090\_COMB.seq:\*  
15: /cgn2\_6/ptodata/2/pna/US091\_COMB.seq:\*  
16: /cgn2\_6/ptodata/2/pna/US092\_COMB.seq:\*  
17: /cgn2\_6/ptodata/2/pna/US093\_COMB.seq:\*  
18: /cgn2\_6/ptodata/2/pna/US094\_COMB.seq:\*  
19: /cgn2\_6/ptodata/2/pna/US095A\_COMB.seq:\*  
20: /cgn2\_6/ptodata/2/pna/US095B\_COMB.seq:\*  
21: /cgn2\_6/ptodata/2/pna/US095C\_COMB.seq:\*  
22: /cgn2\_6/ptodata/2/pna/US095D\_COMB.seq:\*  
23: /cgn2\_6/ptodata/2/pna/US096A\_COMB.seq:\*  
24: /cgn2\_6/ptodata/2/pna/US096B\_COMB.seq:\*  
25: /cgn2\_6/ptodata/2/pna/US096C\_COMB.seq:\*  
26: /cgn2\_6/ptodata/2/pna/US096D\_COMB.seq:\*  
27: /cgn2\_6/ptodata/2/pna/US096E\_COMB.seq:\*  
28: /cgn2\_6/ptodata/2/pna/US097A\_COMB.seq:\*  
29: /cgn2\_6/ptodata/2/pna/US097B\_COMB.seq:\*  
30: /cgn2\_6/ptodata/2/pna/US097C\_COMB.seq:\*  
31: /cgn2\_6/ptodata/2/pna/US098A\_COMB.seq:\*  
32: /cgn2\_6/ptodata/2/pna/US098B\_COMB.seq:\*  
33: /cgn2\_6/ptodata/2/pna/US098C\_COMB.seq:\*  
34: /cgn2\_6/ptodata/2/pna/US099A\_COMB.seq:\*  
35: /cgn2\_6/ptodata/2/pna/US099B\_COMB.seq:\*  
36: /cgn2\_6/ptodata/2/pna/US099C\_COMB.seq:\*  
37: /cgn2\_6/ptodata/2/pna/US099D\_COMB.seq:\*  
38: /cgn2\_6/ptodata/2/pna/US100A\_COMB.seq:\*  
39: /cgn2\_6/ptodata/2/pna/US100B\_COMB.seq:\*  
40: /cgn2\_6/ptodata/2/pna/US101A\_COMB.seq:\*  
41: /cgn2\_6/ptodata/2/pna/US101B\_COMB.seq:\*  
42: /cgn2\_6/ptodata/2/pna/US102A\_COMB.seq:\*  
43: /cgn2\_6/ptodata/2/pna/US102B\_COMB.seq:\*

44: /cgn2\_6/ptodata/2/pna/US6000\_COMB.seq:\*  
45: /cgn2\_6/ptodata/2/pna/US6001\_COMB.seq:\*  
46: /cgn2\_6/ptodata/2/pna/US6002\_COMB.seq:\*  
47: /cgn2\_6/ptodata/2/pna/US6003\_COMB.seq:\*  
48: /cgn2\_6/ptodata/2/pna/US6004\_COMB.seq:\*  
49: /cgn2\_6/ptodata/2/pna/US6005\_COMB.seq:\*  
50: /cgn2\_6/ptodata/2/pna/US6006\_COMB.seq:\*  
51: /cgn2\_6/ptodata/2/pna/US6007\_COMB.seq:\*  
52: /cgn2\_6/ptodata/2/pna/US6008\_COMB.seq:\*  
53: /cgn2\_6/ptodata/2/pna/US6009\_COMB.seq:\*  
54: /cgn2\_6/ptodata/2/pna/US6010\_COMB.seq:\*  
55: /cgn2\_6/ptodata/2/pna/US6011\_COMB.seq:\*  
56: /cgn2\_6/ptodata/2/pna/US6012\_COMB.seq:\*  
57: /cgn2\_6/ptodata/2/pna/US6013\_COMB.seq:\*  
58: /cgn2\_6/ptodata/2/pna/US6014\_COMB.seq:\*  
59: /cgn2\_6/ptodata/2/pna/US6015\_COMB.seq:\*  
60: /cgn2\_6/ptodata/2/pna/US6016\_COMB.seq:\*  
61: /cgn2\_6/ptodata/2/pna/US6017\_COMB.seq:\*  
62: /cgn2\_6/ptodata/2/pna/US6018\_COMB.seq:\*  
63: /cgn2\_6/ptodata/2/pna/US6019\_COMB.seq:\*  
64: /cgn2\_6/ptodata/2/pna/US6020\_COMB.seq:\*  
65: /cgn2\_6/ptodata/2/pna/US6021\_COMB.seq:\*  
66: /cgn2\_6/ptodata/2/pna/US6022\_COMB.seq:\*  
67: /cgn2\_6/ptodata/2/pna/US6023\_COMB.seq:\*  
68: /cgn2\_6/ptodata/2/pna/US6024\_COMB.seq:\*  
69: /cgn2\_6/ptodata/2/pna/US6025\_COMB.seq:\*  
70: /cgn2\_6/ptodata/2/pna/US6026\_COMB.seq:\*  
71: /cgn2\_6/ptodata/2/pna/US6027\_COMB.seq:\*  
72: /cgn2\_6/ptodata/2/pna/US6028\_COMB.seq:\*  
73: /cgn2\_6/ptodata/2/pna/US6029\_COMB.seq:\*  
74: /cgn2\_6/ptodata/2/pna/US6030\_COMB.seq:\*  
75: /cgn2\_6/ptodata/2/pna/US6031\_COMB.seq:\*  
76: /cgn2\_6/ptodata/2/pna/US6032\_COMB.seq:\*  
77: /cgn2\_6/ptodata/2/pna/US6033\_COMB.seq:\*  
78: /cgn2\_6/ptodata/2/pna/US6034\_COMB.seq:\*  
79: /cgn2\_6/ptodata/2/pna/US6035\_COMB.seq:\*  
80: /cgn2\_6/ptodata/2/pna/US6036\_COMB.seq:\*  
81: /cgn2\_6/ptodata/2/pna/US6037\_COMB.seq:\*  
82: /cgn2\_6/ptodata/2/pna/US6038\_COMB.seq:\*  
83: /cgn2\_6/ptodata/2/pna/US6039\_COMB.seq:\*  
84: /cgn2\_6/ptodata/2/pna/US6040\_COMB.seq:\*  
85: /cgn2\_6/ptodata/2/pna/US6041\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	5232	100.0	5232	36	US-09-974-592-3	Sequence 3, Appli
2	2511	48.0	8763	1	PCT-US01-01324-3044	Sequence 3044, Ap
3	2511	48.0	8763	39	US-10-079-979-3044	Sequence 3044, Ap
4	2278	43.5	3000	26	US-09-672-717-231	Sequence 231, App
5	2027	38.7	2404	36	US-09-964-899-38	Sequence 38, Appli
6	1990	38.0	2540	1	PCT-US00-00583-1	Sequence 1, Appli
7	1990	38.0	2540	1	PCT-US02-11757-25	Sequence 25, Appli
8	1990	38.0	2540	1	PCT-US02-11758-25	Sequence 25, Appli
9	1990	38.0	2540	9	US-08-576-956-3	Sequence 3, Appli
10	1990	38.0	2540	9	US-08-576-956A-3	Sequence 3, Appli
11	1990	38.0	2540	14	US-09-011-356-3	Sequence 3, Appli
12	1990	38.0	2540	14	US-09-011-356-3	Sequence 3, Appli
13	1990	38.0	2540	14	US-09-023-655-900	Sequence 219, App
14	1990	38.0	2540	14	US-09-053-375B-219	Sequence 219, App
15	1990	38.0	2540	16	US-09-201-932-3	Sequence 3, Appli
16	1990	38.0	2540	16	US-09-201-932-3	Sequence 3, Appli
17	1990	38.0	2540	16	US-09-201-936-3	Sequence 3, Appli
18	1990	38.0	2540	25	US-09-654-743-3	Sequence 3, Appli
19	1990	38.0	2540	26	US-09-672-717-218	Sequence 218, App
20	1990	38.0	2540	38	US-10-007-926A-274	Sequence 274, App
21	1990	38.0	2540	39	US-10-070-789-1	Sequence 1, Appli









Query Match 48.0%; Score 2511; DB 1; Length 8763;									
Best Local Similarity 99.8%; Pred. No. 0;									
Matches 2881; Conservative 0; Mismatches 5; Indels 1; Gaps 1;									
QY	2344	GGGCGCTTTTCACCTTTCTACCTTTTTCATTTGTTCTGTTCCGAATTTTATAAGTATGTA	2403						
DB	1	GGGCGCTTTTCACCTTTCTACCTTTTTCATTTGTTCTGTTCCGAATTTTATAAGTATGTA	60						
QY	2404	TTACTTTTGTAAACAGAAATTTTAGAAGATTTTCTGATTTAAAGGCTTAGGCATGTT	2463						
DB	61	TTACTTTTGTAAACAGAAATTTTAGAAGATTTTCTGATTTAAAGGCTTAGGCATGTT	120						
QY	2464	CAAAAGCGCTGCAAAACTACTTATCACTACAGCTTTAGTTTCTTAATCCAAAGAGGAGGG	2523						
DB	121	CAAAAGCGCTGCAAAACTACTTATCACTACAGCTTTAGTTTCTTAATCCAAAGAGGAGGG	180						
QY	2524	CAGTTAACCTTTTGGTGCCAAATGTGAATGTAAATGATTTATGTTTTCCTGCTTTGT	2583						
DB	181	CAGTTAACCTTTTGGTGCCAAATGTGAATGTAAATGATTTATGTTTTCCTGCTTTGT	240						
QY	2584	GGATGAAATATTTCTGAGTGTAGTTTTCGACAGGTAGACATCTCTATCTGTTT	2643						
DB	241	GGATGAAATATTTCTGAGTGTAGTTTTCGACAGGTAGACATCTCTATCTGTTT	300						
QY	2644	CAAAATAAGTATTTCTGATTTTGTAAATGAAATATAAAATATGCTFCAGATCTTCCAAT	2703						
DB	301	CAAAATAAGTATTTCTGATTTTGTAAATGAAATATAAAATATGCTFCAGATCTTCCAAT	360						
QY	2704	TAATTAGTAAGATTCATCCTTAATCCTGCTAGTTTAAAGCCGCTTAAGTATGTA	2763						
DB	361	TAATTAGTAAGATTCATCCTTAATCCTGCTAGTTTAAAGCCGCTTAAGTATGTA	420						
QY	2764	AAAAGATCTTTGTTAACTAGTATTTTAAACATCTGTCAGCTTATGTAAGTAAAGTAGA	2823						
DB	421	AAAAGATCTTTGTTAACTAGTATTTTAAACATCTGTCAGCTTATGTAAGTAAAGTAGA	480						
QY	2824	AGCATGTTTGTACACTGCTTGTAGTTATAGTGACAGCTTTTCCATGTTGAGATCTCATAT	2883						
DB	481	AGCATGTTTGTACACTGCTTGTAGTTATAGTGACAGCTTTTCCATGTTGAGATCTCATAT	540						
QY	2884	CATCTGTATCTTAAAGTTTCATGTGAGTTTTCACCGTTAGGATGATTAAGATGATATA	2943						
DB	541	CATCTGTATCTTAAAGTTTCATGTGAGTTTTCACCGTTAGGATGATTAAGATGATATA	600						
QY	2944	GGACAAATGTTAAGCTTTTCCCTACCTACATTTGTTTTCCTGCTAGTAAGTATGTA	3003						
DB	601	GGACAAATGTTAAGCTTTTCCCTACCTACATTTGTTTTCCTGCTAGTAAGTATGTA	660						
QY	3004	GATACTTCTGAAATATAATGTTCTCAAGATCCTTAAACCTCTTGGAAATTTATAAAAT	3063						
DB	661	GATACTTCTGAAATATAATGTTCTCAAGATCCTTAAACCTCTTGGAAATTTATAAAAT	720						
QY	3064	ATTGGCAAGAAAAGAAATAGTTGTTTAAATATTTTAAAAACACTTTGAATAAGAAAT	3123						
DB	721	ATTGGCAAGAAAAGAAATAGTTGTTTAAATATTTTAAAAACACTTTGAATAAGAAAT	780						
QY	3124	CAGTAGGGTATAAAGTATTAAGATTTAAATGCTCATAGAACGTCAGGGTTTACATTTAC	3183						
DB	781	CAGTAGGGTATAAAGTATTAAGATTTAAATGCTCATAGAACGTCAGGGTTTACATTTAC	840						
QY	3184	AAGATTTCTACAAACAAACCCATTTAGAGGTGAGTAAGGATGTTTACTACAGAGGAAAGT	3243						
DB	841	AAGATTTCTACAAACAAACCCATTTAGAGGTGAGTAAGGATGTTTACTACAGAGGAAAGT	900						
QY	3244	TTGAGAGTAAACCTGTAAGAAATATATTTTGTGTACTTTCTTAAGAGAAAGATGATG	3303						
DB	901	TTGAGAGTAAACCTGTAAGAAATATATTTTGTGTACTTTCTTAAGAGAAAGATGATG	960						
QY	3304	TTATGTTCTCCTAACCTTCTGTTACTACTTTAAGTGATATTCATTTAAACATTTGCA	3363						
DB	961	TTATGTTCTCCTAACCTTCTGTTACTACTTTAAGTGATATTCATTTAAACATTTGCA	1020						

QY	3364	AATTTATTTTATTTATTTATTTTCTTTTGAGATGGAGCTTGTCTGTGTCACCCAGGCTG	3423						
DB	1021	AATTTATTTTATTTATTTATTTTCTTTTGAGATGGAGCTTGTCTGTGTCACCCAGGCTG	1080						
QY	3424	GAGTGCAGTGGAGTGATCTCTGCTCACTGCAACCTCGCCCTTCTGGGTTCAAGCGATTC	3483						
DB	1081	GAGTGCAGTGGAGTGATCTCTGCTCACTGCAACCTCGCCCTTCTGGGTTCAAGCGATTC	1140						
QY	3484	CGTGCCCTCAGCTCCCTGAGTAGCTGGAATTTACAGGCAAGTGCCACCATGCCCGACTAAT	3543						
DB	1141	CGTGCCCTCAGCTCCCTGAGTAGCTGGAATTTACAGGCAAGTGCCACCATGCCGACTAAT	1200						
QY	3544	TTTTTTTATTTTAGTAGAGACGGGTTTCCACATGTTGGCCAGGCTGGTATCAAACTCC	3603						
DB	1201	TTTTTTTATTTTAGTAGAGACGGGTTTCCACATGTTGGCCAGGCTGGTATCAAACTCC	1260						
QY	3604	TGACCTCAAGAGATCCACTGCGCTTGCCCTCCCAAGTGTGGGATTTACAGGCTTGAGCC	3663						
DB	1261	TGACCTCAAGAGATCCACTGCGCTTGCCCTCCCAAGTGTGGGATTTACAGGCTTGAGCC	1320						
QY	3664	ACCAGCGCCGGCTAAACATTTGCAAAATTTAAATGAGAGTTTAAATAATTAATGACT	3723						
DB	1321	ACCAGCGCCGGCTAAACATTTGCAAAATTTAAATGAGAGTTTAAATAATTAATGACT	1380						
QY	3724	GCCTGTTTCTGTTTATGATGTAATCCTCAGTCTTTCACCTTTGCACCTGCTGCCACT	3783						
DB	1381	GCCTGTTTCTGTTTATGATGTAATCCTCAGTCTTTCACCTTTGCACCTGCTGCCACT	1440						
QY	3784	TAGTTTGGTTATATAGTCATTAACCTGAATTTGGTCTGTATAGTCTAGACTTTAAATTTA	3843						
DB	1441	TAGTTTGGTTATATAGTCATTAACCTGAATTTGGTCTGTATAGTCTAGACTTTAAATTTA	1500						
QY	3844	AAGTTTCTACAGGGGAGAAAGTGTAAATTTTAAATAATGTTTCCAGCACACT	3903						
DB	1501	AAGTTTCTACAGGGGAGAAAGTGTAAATTTTAAATAATGTTTCCAGCACACT	1560						
QY	3904	CACCTTCCAACTCAGGTAGTGTCAATCTAGTTTGTAGGCAAGGACTCAAGGACTGAAT	3963						
DB	1561	CACCTTCCAACTCAGGTAGTGTCAATCTAGTTTGTAGGCAAGGACTCAAGGACTGAAT	1620						
QY	3964	TGTTTAAACATAGGCTTTTCTGTTCTGGAGCGGCACTTCATTAATTTCTTCTAAAA	4023						
DB	1621	TGTTTAAACATAGGCTTTTCTGTTCTGGAGCGGCACTTCATTAATTTCTTCTAAAA	1680						
QY	4024	CTTGATGTTTATAGGTTAAAGCAAGCTTTTCTTCTCCTCCTCCTGCTGTAATTTA	4083						
DB	1681	CTTGATGTTTATAGGTTAAAGCAAGCTTTTCTTCTCCTCCTCCTGCTGTAATTTA	1740						
QY	4084	ATGCACAACTGATGTGGCTTAAACAGTTTATTTTAAAGAAATGTTTAAAGAAATGCTGTGC	4143						
DB	1741	ATGCACAACTGATGTGGCTTAAACAGTTTATTTTAAAGAAATGTTTAAAGAAATGCTGTGC	1800						
QY	4144	TTCAAGTTCTTAAATCACTCAGCACCTCCAACTTCTAATCAAAATTTTGGAGACTTAACA	4203						
DB	1801	TTCAAGTTCTTAAATCACTCAGCACCTCCAACTTCTAATCAAAATTTTGGAGACTTAACA	1860						
QY	4204	GCATTTCTGCTGTTTGAATATATAAAGCAGCGGATTTTCCATCTAATTTCCGCAAAA	4263						
DB	1861	GCATTTCTGCTGTTTGAATATATAAAGCAGCGGATTTTCCATCTAATTTCCGCAAAA	1920						
QY	4264	ATTGATCATTTGCAAGCTCAAACTATAGCATATCCAAATCTTTTCCCTCCCAAGAG	4323						
DB	1921	ATTGATCATTTGCAAGCTCAAACTATAGCATATCCAAATCTTTTCCCTCCCAAGAG	1980						
QY	4324	TTCTCAGTGTCTACATGTAGACTATTCCTTTTCTGTATAAAGTTTCACTCTAGGATTTCAA	4383						
DB	1981	TTCTCAGTGTCTACATGTAGACTATTCCTTTTCTGTATAAAGTTTCACTCTAGGATTTCAA	2040						
QY	4384	GTCAACACTTATTTTACATTTTAGTCATGCACCAATTTCAAGTAGTTTGCATTAAGTACT	4443						
DB	2041	GTCAACACTTATTTTACATTTTAGTCATGCACCAATTTCAAGTAGTTTGCATTAAGTACT	2100						
QY	4444	TATCTTTTATTTGTAATTAATTTAGTCTGCTGATCAAAAGCAATTTGCTTAATTTTGGAGAC	4503						



QY 3364 AATTATATTTTATTTATTTTCTTTTGTGAGTGGAGTCTTGTCTGTACCCAGGCTG 3423  
Db 1021 AATTTATTTTATTTATTTTCTTTTGTGAGTGGAGTCTTGTCTGTACCCAGGCTG 1080  
QY 3424 GAGTGCAGTGGAGTATCTCTGCTCACTGCAACCTCCGCTTCTGGGTTCAAGCGATTTCT 3483  
Db 1081 GAGTGCAGTGGAGTATCTCTGCTCACTGCAACCTCCGCTTCTGGGTTCAAGCGATTTCT 1140  
QY 3484 CGTGCCTCAGCTTCCCTGAGTGTGGAATACAGGCAGGTGCCACCATCCCGACTAAAT 3543  
Db 1141 CGTGCCTCAGCTTCCCTGAGTGTGGAATACAGGCAGGTGCCACCATCCCGACTAAAT 1200  
QY 3544 TTTTTTATTTTATGAGAGCGGGTTTACCATGTTGGCCAGGCTGGTATCAAACTCC 3603  
Db 1201 TTTTTTATTTTATGAGAGCGGGTTTACCATGTTGGCCAGGCTGGTATCAAACTCC 1260  
QY 3604 TGACCTCAAGAGATCCACTGGCTTGCCTCCCAAGTCTGGGATACAGGCTTGAGCC 3663  
Db 1261 TGACCTCAAGAGATCCACTGGCTTGCCTCCCAAGTCTGGGATACAGGCTTGAGCC 1320  
QY 3664 ACCACGCCGGCTAAACATTTGCAATTTAAATGAGAGTTTAAATAATTAATATGACT 3723  
Db 1321 ACCACGCCGGCTAAACATTTGCAATTTAAATGAGAGTTTAAATAATTAATATGACT 1380  
QY 3724 GCCCTGTTTCTGTTTATGATGTAAATCCTCAGTCTTCCACCTTTGCACTGTCTGCCACT 3783  
Db 1381 GCCCTGTTTCTGTTTATGATGTAAATCCTCAGTCTTCCACCTTTGCACTGTCTGCCACT 1440  
QY 3784 TAGTTTGGTTATATAGTCATTAACTTGGAATTTGGTCTGTATAGTCVAGACTTTAAATTTA 3843  
Db 1441 TAGTTTGGTTATATAGTCATTAACTTGGAATTTGGTCTGTATAGTCVAGACTTTAAATTTA 1500  
QY 3844 AAGTTTCTACAGGGGAGAAAGTCTTAAATTTTAAATATGTTTCCAGGACACTT 3903  
Db 1501 AAGTTTCTACAGGGGAGAAAGTCTTAAATTTTAAATATGTTTCCAGGACACTT 1560  
QY 3904 CACTTCCAAGTCAGGTAGTGTCAATCTAGTTGTAGCCAGGACTCAAGGACTGAAT 3963  
Db 1561 CACTTCCAAGTCAGGTAGTGTCAATCTAGTTGTAGCCAGGACTCAAGGACTGAAT 1620  
QY 3964 TGTTTTTAACATTAAGGCTTTTCTGTTCTGGGAGCCGCACTTCATTAATAATTTCTTAATA 4023  
Db 1621 TGTTTTTAACATTAAGGCTTTTCTGTTCTGGGAGCCGCACTTCATTAATAATTTCTTAATA 1680  
QY 4024 CTGTATGTTTGTAGTGTAAAGCAAGTCTTTTCTTCTCCTCCTCAGTGTGTGAATTTA 4083  
Db 1681 CTGTATGTTTGTAGTGTAAAGCAAGTCTTTTCTTCTCCTCCTCAGTGTGTGAATTTA 1740  
QY 4084 ATGCACAACGCTGATGTGGCTAACAAAGTTTATTTTAAAGAAATGTTTAAAGAAATGCTGTTCG 4143  
Db 1741 ATGCACAACGCTGATGTGGCTAACAAAGTTTATTTTAAAGAAATGTTTAAAGAAATGCTGTTCG 1800  
QY 4144 TTCAGGTTCTTAAATCACTCAGCACTCCAACTTCTTAATCAAAATTTTGGAGACTTTAAACA 4203  
Db 1801 TTCAGGTTCTTAAATCACTCAGCACTCCAACTTCTTAATCAAAATTTTGGAGACTTTAAACA 1860  
QY 4204 GCATTTGCTGTCTTGAACATAAAAGCACCGGATCTTTCCATCTAATCCGCAAAA 4263  
Db 1861 GCATTTGCTGTCTTGAACATAAAAGCACCGGATCTTTCCATCTAATCCGCAAAA 1920  
QY 4264 ATTGATCAATTTGCAAAAGTCAAACTATAGCCATATCCAAATCTTTTCCCTCCCAAGAG 4323  
Db 1921 ATTGATCAATTTGCAAAAGTCAAACTATAGCCATATCCAAATCTTTTCCCTCCCAAGAG 1980  
QY 4324 TTCTCAGTCTACATGTAGACTATTTCTTTCTGTATTAAGTTCATCTAGGATTTCAA 4383  
Db 1981 TTCTCAGTCTACATGTAGACTATTTCTTTCTGTATTAAGTTCATCTAGGATTTCAA 2040  
QY 4384 GTCACCACTTATTTTACATTTTAGTCATCAAGATTCAGTAGTTTTCGAATACTACT 4443  
Db 2041 GTCACCACTTATTTTACATTTTAGTCATCAAGATTCAGTAGTTTTCGAATACTACT 2100  
QY 4444 TATCTTTATTTGTAATAATTTAGTCTGCTGATCAAAAGCATTTGCTTAATTTTGTAGAAC 4503

Db 2101 TATCTTTATTTGTAATAATTTAGTCTGCTGATCAAAAGCATTTGCTTAATTTTGTAGAAC 2160  
QY 4504 TGGTTTTAGCATTTACAACTAAATTTCCAGTTAAATTAATTAAGCTTTATATGCTTTT 4563  
Db 2161 TGGTTTTAGCATTTACAACTAAATTTCCAGTTAAATTAATTAAGCTTTATATGCTTTT 2220  
QY 4564 CTTGCTACATTTGGTTTTTTTCCCTCTCCCTTTGATTAAGGGCTAAGGTAAGANN 4623  
Db 2221 CTTGCTACATTTGGTTTTTTTCCCTCTCCCTTTGATTAAGGGCTAAGGTAAGG - AGAGT 2279  
QY 4624 GGGTGTAGTGTATATAATGTGATTTGGCCCTGTGATTAATGATATTTTGTATTTT 4683  
Db 2280 GGGTGTAGTGTATATAATGTGATTTGGCCCTGTGATTAATGATATTTTGTATTTT 2339  
QY 4684 TGTGTTATATTTATTTACATTTTCAGTGTGTTTTTGTGTTTCCATTTTAGGGGATAA 4743  
Db 2340 TGTGTTATATTTATTTACATTTTCAGTGTGTTTTTGTGTTTCCATTTTAGTGAATA 2399  
QY 4744 ATTTGTATTTTGAACATATGAATGGAGACTACCGCCCGCAGCATTTGTTTACATGATATAC 4803  
Db 2400 ATTTGTATTTTGNACTATGAATGGAGACTACCGCCCGCAGCATTTGTTTACATGATATAC 2459  
QY 4804 CCTTTAAACCCGAATCATTTGTTTTTATTTCTGATTACACAGTGTGTTGAATGGGAAAGG 4863  
Db 2460 CCTTTAAACCCGAATCATTTGTTTTTATTTCTGATTACACAGTGTGTTGAATGGGAAAGG 2519  
QY 4864 GCTAGTATATCAGTAGGATATACTATGGGATGTATATATATCATTTGTTTACAGAAATG 4923  
Db 2520 GCTAGTATATCAGTAGGATATACTATGGGATGTATATATATCATTTGTTTACAGAAATG 2579  
QY 4924 AAATAAATGGGCTGGGCTCAGTGGCTCAGGCTCTAATCCCGAGCATTTTGGGAGGCTG 4983  
Db 2580 AAATAAATGGGCTGGGCTCAGTGGCTCAGGCTCTAATCCCGAGCATTTTGGGAGGCTG 2639  
QY 4984 AGSCAGTGGATACAGAGTTCAGGAGTTCAGACCATCTCTGGCTTAACACGGTGAACCC 5043  
Db 2640 AGSCAGTGGATACAGAGTTCAGGAGTTCAGACCATCTCTGGCTTAACACGGTGAACCC 2699  
QY 5044 GTCTCTACTAAAAACAGAAATTTAGCCGGGCTGTAGCCGGGCGCTGTAGTCCAGCT 5103  
Db 2700 GTCTCTACTAAAAACAGAAATTTAGCCGGGCTGTAGCCGGGCGCTGTAGTCCAGCT 2759  
QY 5104 ACTCGGAGGCTGAGCAGGAGAAATGTTGTAACCCGGGAGGAGAGTTCAGTGTAGCC 5163  
Db 2760 ACTCGGAGGCTGAGCAGGAGAAATGTTGTAACCCGGGAGGAGAGTTCAGTGTAGCC 2819  
QY 5164 GAGATCTGCCACTGCACTCCAGCTGGGCAACAGAGCAAGACTCTGTCTCAAAAAAAA 5223  
Db 2820 GAGATCTGCCACTGCACTCCAGCTGGGCAACAGAGCAAGACTCTGTCTCAAAAAAAA 2879  
QY 5224 AAAAAA 5230  
Db 2880 AAAAAA 2886

RESULT 4  
US-09-672-717-231  
; Sequence 231, Application US/09672717  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G.  
; APPLICANT: LaCasse, Eric  
; APPLICANT: Baird, Stephen  
; APPLICANT: Holcik, Martin  
; APPLICANT: Young, Sean  
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses  
; FILE REFERENCE: 07891/025001  
; CURRENT APPLICATION NUMBER: US/09/672,717  
; CURRENT FILING DATE: 2000-09-28  
; NUMBER OF SEQ ID NOS: 231  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 231

QY	961	TGGAGGCCCGAGTGAAGACCCCTTGGGAAACAACATGCTTAATGTATGCACGGGTGCAAAATAT	1072
DB	1617	TGGAGGCCCGAGTGAAGACCCCTTGGGAAACAACATGCTTAATGTATGCACGGGTGCAAAATAT	1676
QY	1021	CTGTTTAGAACAGAAGGACAGAATAATATAAACAATATTATTCAITTTAACTTCATTCACTTGAG	1080
DB	1677	CTGTTTAGAACAGAAGGACAGAATAATATAAACAATATTATTCAITTTAACTTCATTCACTTGAG	1736
QY	1081	GAGTGTCTGTTTAAGAACTACTGAGAAAAACACCATCACTAACTTAGAAGAAITTTGATGATACC	1140
DB	1737	GAGTGTCTGTTTAAGAACTACTGAGAAAAACACCATCACTAACTTAGAAGAAITTTGATGATACC	1796
QY	1141	ATCTTCCAANAATCCTATFGGTACAAGAAGCTATACGAATGGGGTTCAGTTTCAAGACAAATT	1200
DB	1797	ATCTTCCAANAATCCTATFGGTACAAGAAGCTATACGAATGGGGTTCAGTTTCAAGACAAATT	1856
QY	1201	AAGAAAATAATGGAGGAAAAAATTCAGATATCTGGGAGCAACTATATAAATCACTTCAGGTT	1260
DB	1857	AAGAAAATAATGGAGGAAAAAATTCAGATATCTGGGAGCAACTATATAAATCACTTCAGGTT	1916
QY	1261	CTGTTTGCAGATCTAGTGAATGCTCAGAAGACAGCATATCAAGATGAGTCAAGTCAGACT	1320
DB	1917	CTGTTTGCAGATCTAGTGAATGCTCAGAAGACAGCATATCAAGATGAGTCAAGTCAGACT	1976
QY	1321	TCATTACAGAAAGAGATTAGTACTGAAGAGCAGCTAAGGGCCCTGCAAGAGAGAGAAGCTT	1380
DB	1977	TCATTACAGAAAGAGATTAGTACTGAAGAGCAGCTAAGGGCCCTGCAAGAGAGAGAAGCTT	2036
QY	1381	TGCAAAATCTGTATGGATAGAAATATTGCTATCGTTTTTTTGTTCCTGTGGCACCTAGTC	1440
DB	2037	TGCAAAATCTGTATGGATAGAAATATTGCTATCGTTTTTTTGTTCCTGTGGCACCTAGTC	2096
QY	1441	ACTTGTAAACAATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGTCATTACT	1500
DB	2097	ACTTGTAAACAATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGTCATTACT	2156
QY	1501	TTCAGCAAAAATTTTTATGCTCTTAATCTAATCTATAGTAGGCATGTTATGTTGTTCT	1560
DB	2157	TTCAGCAAAAATTTTTATGCTCTTAATCTAATCTATAGTAGGCATGTTATGTTGTTCT	2216
QY	1561	TATTTACCCCTGATTGAATGCTGTGATGTGAACCTGACTTTTAGTAAATCAGGATTCGAATCCAT	1620
DB	2217	TATTTACCCCTGATTGAATGCTGTGATGTGAACCTGACTTTTAGTAAATCAGGATTCGAATCCAT	2276
QY	1621	TAGCATTTTGCTTACCAAGTAGGAAAAAATGTACATGGCAGTGTTTTACTTGGCAATAATA	1680
DB	2277	TAGCATTTTGCTTACCAAGTAGGAAAAAATGTACATGGCAGTGTTTTACTTGGCAATAATA	2336
QY	1681	ATCTTTGAAATTCCTGATTTTTTCAGGCTATTAGCTGCTATTATCCATTTTTTTTACTGTTA	1740
DB	2337	ATCTTTGAAATTCCTGATTTTTTCAGGCTATTAGCTGCTATTATCCATTTTTTTTACTGTTA	2396
QY	1741	TTTAAATTGAAACCATAGACTTAAGAAATAAGAGCATCACTATTAACCTGAACACAATGTGT	1800
DB	2397	TTTAAATTGAAACCATAGACTTAAGAAATAAGAGCATCACTATTAACCTGAACACAATGTGT	2456
QY	1801	ATTCATAGTACTACTGATTTAAATTTCTTAAGTGAAGTGAATTAATCATCTCGAATTTTTTAT	1860
DB	2457	ATTCATAGTACTACTGATTTAAATTTCTTAAGTGAAGTGAATTAATCATCTCGAATTTTTTAT	2516
QY	1861	TCTTTTTCAGATAGGCTTTAACAATGGAGCTTTCGTATATAAATCTGGAGATTAGAGTTA	1920
DB	2517	TCTTTTTCAGATAGGCTTTAACAATGGAGCTTTCGTATATAAATCTGGAGATTAGAGTTA	2576
QY	1921	ATCTCCCCAATCATATAATTTGTTTCTGTGAAAAAGGAATAAATGTTTCCATGCTGGTG	1980
DB	2577	ATCTCCCCAATCATATAATTTGTTTCTGTGAAAAAGGAATAAATGTTTCCATGCTGGTG	2636
QY	1981	GAAGATAGAGATTGTTTTTAGAGTTGGTGTGTTTTTAGGATTCGTGCCATTTTTCT	2040
DB	2637	GAAGATAGAGATTGTTTTTAGAGTTGGTGTGTTTTTAGGATTCGTGCCATTTTTCT	2696
QY	2041	TTTTAAAGTTATAACACGCTACTTGTGCGAAATATATTTTTTAAAGTGATTTGCGCAATTTTG	2100

Query Match	43.5%	Score 2278;	DB 26;	Length 3000;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2328;	Conservative	0;	Mismatches 1;	Indels 0; Gaps
QY	1	GAAGAAGTGGACAAAGTCCTATTTTCAAGAGAGATGACTTTTAACAGTGTGTTGAAGAGTCT	60	
DB				
QY	657	GAAGAAGTGGACAAAGTCCTATTTTCAAGAGAGATGACTTTTAACAGTGTGTTGAAGAGTCT	716	
DB				
QY	61	AAAACTTGTACCTGCGACACATCAATTAAGGAAGAAGAAATTTGTAGAAGAGTGTAAATAGA	120	
DB				
QY	717	AAAACTTGTACCTGCGACACATCAATTAAGGAAGAAGAAATTTGTAGAAGAGTGTAAATAGA	776	
DB				
QY	121	TTAAAAACTTTGGCTAAATTTTCCAAGTGGTAGTCTGTTTTCAGCATCAACACTGGCAGCA	180	
DB				
QY	777	TTAAAAACTTTGGCTAAATTTTCCAAGTGGTAGTCTGTTTTCAGCATCAACACTGGCAGCA	836	
DB				
QY	181	GCAGGGTTTCTTTATACTGGTGAAGGAGATACCGTGCGGTGCTTTAGTTGTTCATGCAGCT	240	
DB				
QY	837	GCAGGGTTTCTTTATACTGGTGAAGGAGATACCGTGCGGTGCTTTAGTTGTTCATGCAGCT	896	
DB				
QY	241	GTAGATAGATGGCAATPATGGAGACTCAGCAGTTGGAAGACACAGGAAGTAGTATCCCCAAAT	300	
DB				
QY	897	GTAGATAGATGGCAATPATGGAGACTCAGCAGTTGGAAGACACAGGAAGTAGTATCCCCAAAT	956	
DB				
QY	301	TGCAGATTTTCAACGGCTTTTATCTTGAANAATAGTGCACGCAGCTTACAAATCTGGT	360	
DB				
QY	957	TGCAGATTTTCAACGGCTTTTATCTTGAANAATAGTGCACGCAGCTTACAAATCTGGT	1016	
DB				
QY	361	ATCCGAATGGTTCAGTACAAAGTTGAAAACATATCTCGGAAGCAGAGATCATTTTGCCTTA	420	
DB				
QY	1017	ATCCGAATGGTTCAGTACAAAGTTGAAAACATATCTCGGAAGCAGAGATCATTTTGCCTTA	1076	
DB				
QY	421	GACAGGCCATCTGAGACACATGCAGACTATCTTTTGAGAACTGGGCGAGGTTGTAGATATA	480	
DB				
QY	1077	GACAGGCCATCTGAGACACATGCAGACTATCTTTTGAGAACTGGGCGAGGTTGTAGATATA	1136	
DB				
QY	481	TCAGACACCATATACCCGAGGAGACCTCGCATGTATAGTGAAGAGCTAGATATAAAGTCC	540	
DB				
QY	1137	TCAGACACCATATACCCGAGGAGACCTCGCATGTATAGTGAAGAGCTAGATATAAAGTCC	1196	
DB				
QY	541	TTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTCTGGGACTC	600	
DB				
QY	1197	TTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTCTGGGACTC	1256	
DB				
QY	601	TACTACACAGGTATTTGGTGACCAAGTGCAAGTGCTTTTGTGTGGTGGAATACTGAAAAT	660	
DB				
QY	1257	TACTACACAGGTATTTGGTGACCAAGTGCAAGTGCTTTTGTGTGGTGGAATACTGAAAAT	1316	
DB				
QY	661	TGGGAACCTTGTGATCGTCCCTGGTCAGAAACACAGGCACACTTTTCCTTAATTTGCTCTTT	720	
DB				
QY	1317	TGGGAACCTTGTGATCGTCCCTGGTCAGAAACACAGGCACACTTTTCCTTAATTTGCTCTTT	1376	
DB				
QY	721	GTTTTGGGCGGAACTTAAATATTCGAAGTGAATCTGATGCTGTGAGTCTGTATAGGAAT	780	
DB				
QY	1377	GTTTTGGGCGGAACTTAAATATTCGAAGTGAATCTGATGCTGTGAGTCTGTATAGGAAT	1436	
DB				
QY	781	TTCCCAAAATTCACAAATCTTCCAGAAATCCATCCATGGCAGATTATGAAGACGGATC	840	
DB				
QY	1437	TTCCCAAAATTCACAAATCTTCCAGAAATCCATCCATGGCAGATTATGAAGACGGATC	1496	
DB				
QY	841	TTTACTTTTGGGACATGGATATACTCAGTTTACAAGGAGCAGCTTTCGAAGAGCTGGATTT	900	
DB				
QY	1497	TTTACTTTTGGGACATGGATATACTCAGTTTACAAGGAGCAGCTTTCGAAGAGCTGGATTT	1556	
DB				
QY	901	TATGCTTTTAGGTGAAGGTGATAAAGTAAAGTGTCTTCTACTGTGGAGGAGGCTAACTGAT	960	
DB				
QY	1557	TATGCTTTTAGGTGAAGGTGATAAAGTAAAGTGTCTTCTACTGTGGAGGAGGCTAACTGAT	1616	
DB				







Qy	1500	TTTTCAAGCAAAAAATTTTTATGCTCTTAATCTAACTCTATAGTGGCATGTTATGTTGTC	1559
Db	1501	TTTTCAAGCAAAAAATTTTTATGCTCTTAATCTAACTCTATAGTGGCATGTTATGTTGTC	1560
Qy	1560	TTATTACCCGTGATTGAATGTGTGATGTGAACGTACTTTAAGCTAACTCAGGATTGAATTC	1619
Db	1561	TTATTACCCGTGATTGAATGTGTGATGTGAACGTACTTTAAGCTAACTCAGGATTGAATTC	1620
Qy	1620	TTAGCATTTTGCTACCAAGTAGGAAAAAATGTACATGGCAGTGTTTTAGTGTGCAATAT	1679
Db	1621	TTAGCATTTTGCTACCAAGTAGGAAAAAATGTACATGGCAGTGTTTTAGTGTGCAATAT	1680
Qy	1680	AATCTTTGAAATTTCTTGATTTTTCAGGTTATAGCTGTATATCCATTTTTTTTAC	1739
Db	1681	AATCTTTGAAATTTCTTGATTTTTCAGGTTATAGCTGTATATCCATTTTTTTTAC	1740
Qy	1740	ATTTAATTGAACCATAGACTAAGAAATGAAGAGCATCATCTATAACTGAACACAAGTG	1799
Db	1741	ATTTAATTGAACCATAGACTAAGAAATGAAGAGCATCATCTATAACTGAACACAAGTG	1800
Qy	1800	TATTCATAGTATACTGATTTAATTTCTAAGTGAAGTGAATTAATCATCTGGATTTTTA	1859
Db	1801	TATTCATAGTATACTGATTTAATTTCTAAGTGAAGTGAATTAATCATCTGGATTTTTA	1860
Qy	1860	TTCTTTTCAGATAGGCTTAACAAATGGAGCTTCTGTATATAAATGTGGAGATTAGAGTT	1919
Db	1861	TTCTTTTCAGATAGGCTTAACAAATGGAGCTTCTGTATATAAATGTGGAGATTAGAGTT	1920
Qy	1920	AACTCCCCCAATCACATAATTTGTTTGTCGTAAGAAAGAAATAAATCTCTCCATGCTGGT	1979
Db	1921	AACTCCCCCAATCACATAATTTGTTTGTCGTC- AAAGAGAAATAAATGTTCCATGCTGGT	1979
Qy	1980	GGAAGATAGAGATGCTTTTATAGAGTTGGTTGTTGCTTTTAGGATTCGTCTCAATTTTC	2039
Db	1980	GGAAGATAGAGATGCTTTTATAGAGTTGGTTGTTGCTTTTAGGATTCGTCTCAATTTTC	2039
Qy	2040	TTTTAAAGTTATAAACACGCTACTGTGGCAATATTTTTTTAAAGTGAATTTGCCATTTT	2099
Db	2040	TTTTAAAGTTATAAACACGCTACTGTGGCAATATTTTTTTAAAGTGAATTTGCCATTTT	2099
Qy	2100	GAAAGCGTATTTAATGATAGAATACTATCGAGCCCAACATGACTGACATGGAAAGATGTC	2159
Db	2100	GAAAGCGTATTTAATGATAGAATACTATCGAGCCCAACATGACTGACATGGAAAGATGTC	2159
Qy	2160	AAAGATATGTTAGTGTAAATGCAAGTGGCAAAACACTATGTATAGTCTGAGCCAGATC	2219
Db	2160	AAAGATATGTTAGTGTAAATGCAAGTGGCAAAACACTATGTATAGTCTGAGCCAGATC	2219
Qy	2220	AAAGTATGATGTTTTTAAATATGATAGAAACAAAAAGATTTGGAAGATATACACCAACT	2279
Db	2220	AAAGTATGATGTTTTTAAATATGATAGAAACAAAAAGATTTGGAAGATATACACCAACT	2279
Qy	2280	GTTAAATGCTGGTTTCTCTCGGGAGGGGGGATTTGGGG	2319
Db	2280	GTTAAATGCTGGTTTCTCTCGGGAGGGGGGATTTGGGG	2319

```

RESULT 6
PCT-US00-00583-1
; Sequence 1, Application PC/TUS0000583
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Lex M. Cowser
; APPLICANT: ISTS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS EXPRESSION
; FILE REFERENCE: RTSP-0048
; CURRENT APPLICATION NUMBER: PCT/US00/00583
; CURRENT FILING DATE: 2000-01-10
; EARLIER APPLICATION NUMBER: US 09/392,580
; EARLIER FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1

```

```

; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (34)..(1527)
PCT-US00-00583-1

Query Match      38.0%;   Score 1990;   DB 1;   Length 2540;
Best Local Similarity 100.0%;   Pred. No. 0;
Matches 2040;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy 1  GAAAGGTGGACAAGTCCTATTTTCAAGAGAGAGATGACTTTTAAACAGATTTTGAAGGATCT 60
Db 1  GAAAGGTGGACAAGTCCTATTTTCAAGAGAGAGATGACTTTTAAACAGATTTTGAAGGATCT 60

Qy 61  AAAACTTGTGACCTGCGACAGATCAATAAAGGAAGAAGAAATTTGTAGAAGAGTTTAATAGA 120
Db 61  AAAACTTGTGACCTGCGACAGATCAATAAAGGAAGAAGAAATTTGTAGAAGAGTTTAATAGA 120

Qy 121  TAAAAACCTTTTGCTAAATTTTCCRAGTGGTAGTCCTGTTTCAGCATCAACACTGGCAGGA 180
Db 121  TAAAAACCTTTTGCTAAATTTTCCRAGTGGTAGTCCTGTTTCAGCATCAACACTGGCAGGA 180

Qy 181  CGAGGGTTCTTTATACCTGGTGAAGGAGATACCGTGCAGTGTAGTGTGTCATGCGAGCT 240
Db 181  CGAGGGTTCTTTATACCTGGTGAAGGAGATACCGTGCAGTGTAGTGTGTCATGCGAGCT 240

Qy 241  GTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAAGACACAGAGAAAGTATCCCCAAAT 300
Db 241  GTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAAGACACAGAGAAAGTATCCCCAAAT 300

Qy 301  TGCAGATTATCAACGGCTTTTATCTTGAAATAGTGCACCGCAGCTCTACAAATTCCTGCT 360
Db 301  TGCAGATTATCAACGGCTTTTATCTTGAAATAGTGCACCGCAGCTCTACAAATTCCTGCT 360

Qy 361  ATCCAGAATGGTGCAGTACAAAAGTTGAAAACATCTCTGGGAAGCAGAGATCAITTTGCCCTTA 420
Db 361  ATCCAGAATGGTGCAGTACAAAAGTTGAAAACATCTCTGGGAAGCAGAGATCAITTTGCCCTTA 420

Qy 421  GACAGGCCATCTGAGACACATGCGAGACTATCTTTTGAGAACTGGCGAGGTTGTAGATATA 480
Db 421  GACAGGCCATCTGAGACACATGCGAGACTATCTTTTGAGAACTGGCGAGGTTGTAGATATA 480

Qy 481  TCAGACACCATATACCCAGGAACCTGCCATGTATAGTGAAGAGCTAGATTTAAAGTCC 540
Db 481  TCAGACACCATATACCCAGGAACCTGCCATGTATAGTGAAGAGCTAGATTTAAAGTCC 540

Qy 541  TTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTCTGGAGCTC 600
Db 541  TTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTCTGGAGCTC 600

Qy 601  TACTACAGAGTATTTGTTGACCAAGTCAGTGCATTTTGTGTGGGAAAACTGAAAAAT 660
Db 601  TACTACAGAGTATTTGTTGACCAAGTCAGTGCATTTTGTGTGGGAAAACTGAAAAAT 660

Qy 661  TGGNACCTTTGTATCGTGCCTGGTCAGAACACAGCGGCACACTTTCCTAATTGCTCTTT 720
Db 661  TGGNACCTTTGTATCGTGCCTGGTCAGAACACAGCGGCACACTTTCCTAATTGCTCTTT 720

Qy 721  GTTTTGGCCCGGAATCTTAAATATTCGAAGTGAATCTGATGCTGTGAGTCTGTAGAGGAAT 780
Db 721  GTTTTGGCCCGGAATCTTAAATATTCGAAGTGAATCTGATGCTGTGAGTCTGTAGAGGAAT 780

Qy 781  TTCCCAAAATCAACAAATCTTCCAAAGAAATCCATCCATGGCAGATTAATGAAGCACGGATC 840
Db 781  TTCCCAAAATCAACAAATCTTCCAAAGAAATCCATCCATGGCAGATTAATGAAGCACGGATC 840

Qy 841  TTTACTTTTGGACATGGAATATACTCAGTTTAAACAGGAGCAGCTTGCAGAGCTTGGATTT 900
Db 841  TTTACTTTTGGACATGGAATATACTCAGTTTAAACAGGAGCAGCTTGCAGAGCTTGGATTT 900

Qy 901  TATGCTTTAGGTGAAGGTGATAAAGTAAAGTGTCTTTACTGTGGAGGAGGCTAACTGAT 960

```

Db 901 |||||TATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCCTTTACGTGTGGAGGGGCTAACTGAT 960  
Qy 961 TCGAAGCCAGTGAAGACCTTTGGGAACAACATGCTAAATGCTATCCAGGGTGCATAAT 1020  
Db 961 TCGAAGCCAGTGAAGACCTTTGGGAACAACATGCTAAATGCTATCCAGGGTGCATAAT 1020  
Qy 1021 CTGTTAGAACAGAGGAGCAAGAATATATAACAATATTCATTAACTCACTTCTGAG 1080  
Db 1021 CTGTTAGAACAGAGGAGCAAGAATATATAACAATATTCATTAACTCACTTCTGAG 1080  
Qy 1081 GAGTCTGTGTAAGAACTACTGAGAAAACACCATCACTAAGTAAGAAATTCATATACC 1140  
Db 1081 GAGTCTGTGTAAGAACTACTGAGAAAACACCATCACTAAGTAAGAAATTCATATACC 1140  
Qy 1141 ATCTTCCAAAATCCCTATGTTGTAAGAAGCTATACAAATGGGGTTCAGTTTCAAGGACATT 1200  
Db 1141 ATCTTCCAAAATCCCTATGTTGTAAGAAGCTATACAAATGGGGTTCAGTTTCAAGGACATT 1200  
Qy 1201 AAGAAATTAATGGAGAAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTGAAGTT 1260  
Db 1201 AAGAAATTAATGGAGAAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTGAAGTT 1260  
Qy 1261 CTGGTTGCAGATCTAGTGAATGCTCAGAAAACAGATATGCAAGATCAGTCAAGTCAAGT 1320  
Db 1261 CTGGTTGCAGATCTAGTGAATGCTCAGAAAACAGATATGCAAGATCAGTCAAGTCAAGT 1320  
Qy 1321 TCATTACAGAAAGAGATAGTACTCAAGAGCAGCTAAGGCGCTCAAGAGGAGAGCTT 1380  
Db 1321 TCATTACAGAAAGAGATAGTACTCAAGAGCAGCTAAGGCGCTCAAGAGGAGAGCTT 1380  
Qy 1381 TGCAAAATCTGATGGATAGAAATATGCTATCGTTTTTTTCTGTTGGACATCTAGTC 1440  
Db 1381 TGCAAAATCTGATGGATAGAAATATGCTATCGTTTTTTTCTGTTGGACATCTAGTC 1440  
Qy 1441 ACTTGTAAACAATGTGTAAGCAAGTGTGACAAGTGTCCCATGTGCTTACACATCTACT 1500  
Db 1441 ACTTGTAAACAATGTGTAAGCAAGTGTGACAAGTGTCCCATGTGCTTACACATCTACT 1500  
Qy 1501 TTCAAGCAAAAATTTTATGTCCTTAATCTAACTCTATAGTAGGATGTATGTTGTTCT 1560  
Db 1501 TTCAAGCAAAAATTTTATGTCCTTAATCTAACTCTATAGTAGGATGTATGTTGTTCT 1560  
Qy 1561 TATTACCTGATTTGATGTGATGTGAACCTGACCTTAACTAATCAGGATTTGAAATCCAT 1620  
Db 1561 TATTACCTGATTTGATGTGATGTGAACCTGACCTTAACTAATCAGGATTTGAAATCCAT 1620  
Qy 1621 TAGCATTTGCTACCAAGTAGGAAAAAATGTACATGGCAGTGTGTTTGTGGCAATATA 1680  
Db 1621 TAGCATTTGCTACCAAGTAGGAAAAAATGTACATGGCAGTGTGTTTGTGGCAATATA 1680  
Qy 1681 ATCTTTGAATTTCTGATTTTCAGGGTATTAGCTGTATATCCATTTTTTTTACTGTGA 1740  
Db 1681 ATCTTTGAATTTCTGATTTTCAGGGTATTAGCTGTATATCCATTTTTTTTACTGTGA 1740  
Qy 1741 TTTAATTGAACCATAGACTAAGAAATGAAGACATCACTAATCACTGAACACAATGTGT 1800  
Db 1741 TTTAATTGAACCATAGACTAAGAAATGAAGACATCACTAATCACTGAACACAATGTGT 1800  
Qy 1801 ATTATAGTAACTGATTTAATTTCTAAGTGTAAAGTAATTAATCATCTGGAATTTTTAT 1860  
Db 1801 ATTATAGTAACTGATTTAATTTCTAAGTGTAAAGTAATTAATCATCTGGAATTTTTAT 1860  
Qy 1861 TCTTTTCAGATAGGCTTAAACAATGGAGCTTCTGTATATAAATGTTGGAGATTAGAGTTA 1920  
Db 1861 TCTTTTCAGATAGGCTTAAACAATGGAGCTTCTGTATATAAATGTTGGAGATTAGAGTTA 1920  
Qy 1921 ATCTCCCAATCACATAATTTCTGTTGTAAGAAAGAAATAAATGTTTCCATGCTGGTG 1980  
Db 1921 ATCTCCCAATCACATAATTTCTGTTGTAAGAAAGAAATAAATGTTTCCATGCTGGTG 1980  
Qy 1981 GAAAGATAGAGATTTGTTTAGAGGTGGTGTGTTTGGTGTAGGATTTCTGTCATTTTCT 2040  
Db 1981 GAAAGATAGAGATTTGTTTAGAGGTGGTGTGTTTGGTGTAGGATTTCTGTCATTTTCT 2040

Db 1981 GAAAGATAGAGATTTGTTTAGAGGTGGTGTGTTTGGTGTAGGATTTCTGTCATTTTCT 2040  
Qy 2041 T 2041  
Db 2041 T 2041  
RESULT 7  
PCT-US02-11757-25  
; Sequence 25, Application PC/TUS0211757  
; GENERAL INFORMATION:  
; APPLICANT: PTC Therapeutics, Inc.  
; TITLE OF INVENTION: METHODS FOR IDENTIFYING SMALL MOLECULES THAT BIND SPECIFIC RNA  
; FILE REFERENCE: 10589-007-228  
; CURRENT APPLICATION NUMBER: PCT/US02/11757  
; CURRENT FILING DATE: 2002-04-11  
; PRIOR APPLICATION NUMBER: 60/282,965  
; PRIOR FILING DATE: 2001-04-11  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 25  
; LENGTH: 2540  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-11757-25

Query Match 38.0%; Score 1990; DB 1; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAAAGGTGGACAAGTCCTATTTTCAAGAGAAGATGACATTTTAAACAGTGTGAAAGATCT 60  
Db 1 GAAAAGGTGGACAAGTCCTATTTTCAAGAGAAGATGACATTTTAAACAGTGTGAAAGATCT 60  
Qy 61 AAAACTTGTGTACCTGCAGACATCAATAAGGAAGAAATTTGTAGAAGATTTTAATAGA 120  
Db 61 AAAACTTGTGTACCTGCAGACATCAATAAGGAAGAAATTTGTAGAAGATTTTAATAGA 120  
Qy 121 TTAANAACCTTTTCTTAATTTTCCAGTGGTAGTCCCTGTTTCAGCATCAACACTGGCACCA 180  
Db 121 TTAANAACCTTTTCTTAATTTTCCAGTGGTAGTCCCTGTTTCAGCATCAACACTGGCACCA 180  
Qy 181 GCAGGTTTCTTTATACTGTTGAAGAGATACCGTGGGTGCTTTAGTTGTCTATGCAGCT 240  
Db 181 GCAGGTTTCTTTATACTGTTGAAGAGATACCGTGGGTGCTTTAGTTGTCTATGCAGCT 240  
Qy 241 GTAGATAGATGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAAGTATCCCCAAAT 300  
Db 241 GTAGATAGATGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAAGTATCCCCAAAT 300  
Qy 301 TGCAGATTTTATCAACGGCTTTTATCTTGAANAATAGTCCACGAGTCTACAAATTTCTG 360  
Db 301 TGCAGATTTTATCAACGGCTTTTATCTTGAANAATAGTCCACGAGTCTACAAATTTCTG 360  
Qy 361 ATCCAGAATGGTCAAGTACAAAGTTGAAAACATCTCGGGAAGCAGAGATCATTTGCTTTA 420  
Db 361 ATCCAGAATGGTCAAGTACAAAGTTGAAAACATCTCGGGAAGCAGAGATCATTTGCTTTA 420  
Qy 421 GACAGGCCATCTGAGACACATGCAGACTATCTTTTGAACCTGGGAGGTTGTAGATATA 480  
Db 421 GACAGGCCATCTGAGACACATGCAGACTATCTTTTGAACCTGGGAGGTTGTAGATATA 480  
Qy 481 TCAGACACCATATACCCGAGGACCTGCCATGTATAGTGAAGAACTAGATTAAGTCC 540  
Db 481 TCAGACACCATATACCCGAGGACCTGCCATGTATAGTGAAGAACTAGATTAAGTCC 540  
Qy 541 TTTTCAAGAACTGGCAGACTATGCTACCTAACCCCAAGAGAGTTAGCAAGTCTGGACTC 600  
Db 541 TTTTCAAGAACTGGCAGACTATGCTACCTAACCCCAAGAGAGTTAGCAAGTCTGGACTC 600  
Qy 601 TACTACACAGGTATTTGTTGACCAAGTGCAGTGTGTTTGTGTTGGTGGAAAACCTGAAAAT 660  
Db 601 TACTACACAGGTATTTGTTGACCAAGTGCAGTGTGTTTGTGTTGGTGGAAAACCTGAAAAT 660

```
Db 601 TACTACACAGGTANTGGTGACCAAGTCAGTGTCTTTTGTGTGGTGAAGAACTGAAAAAT 660
QY 661 TGGGAACCTTGTGATCGTCTGCTGAGAACACAGAGGACACTTTCCTAAATTCGCTCTTT 720
Db 661 TGGGAACCTTGTGATCGTCTGCTGAGAACACAGAGGACACTTTCCTAAATTCGCTCTTT 720
QY 721 GTTTTGGCCGGAATCTTAATATATCGAAGTGAATCTGATGCTGTGAGTCTCTGATAGGAAT 780
Db 721 GTTTTGGCCGGAATCTTAATATATCGAAGTGAATCTGATGCTGTGAGTCTCTGATAGGAAT 780
QY 781 TTCCCAAAATTCACAAATCTTCCAGAAATCCATCCATGGCAGATATGAAGCACGGATC 840
Db 781 TTCCCAAAATTCACAAATCTTCCAGAAATCCATCCATGGCAGATATGAAGCACGGATC 840
QY 841 TTTACTTTTGGGACATGATATACTACTAGTTTAAAGGAGCAGCTGCAAGAGCTGGATTT 900
Db 841 TTTACTTTTGGGACATGATATACTACTAGTTTAAAGGAGCAGCTGCAAGAGCTGGATTT 900
QY 901 TATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTTCACTGTGGAGGAGGCTAACTGAT 960
Db 901 TATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTTCACTGTGGAGGAGGCTAACTGAT 960
QY 961 TGGAGCCCAAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCAATAT 1020
Db 961 TGGAGCCCAAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCAATAT 1020
QY 1021 CTGTTAGAACAAGGACAGAAATATATAACAATATTCATTTAACTCATTCACCTTGAG 1080
Db 1021 CTGTTAGAACAAGGACAGAAATATATAACAATATTCATTTAACTCATTCACCTTGAG 1080
QY 1081 GAGTGTCTGTAGAAGTACTAGAGAAACACCATCATCTAACTAGAGAAATGATGATACC 1140
Db 1081 GAGTGTCTGTAGAAGTACTAGAGAAACACCATCATCTAACTAGAGAAATGATGATACC 1140
QY 1141 ATCTTCCAAATCCTATGGTACAGAGCTATACGATGGGTTTCAGTTTCAAGGACATT 1200
Db 1141 ATCTTCCAAATCCTATGGTACAGAGCTATACGATGGGTTTCAGTTTCAAGGACATT 1200
QY 1201 AAGAAATATGAGGAAAAAATTCAGATATCTGGGAGCACTATAAATCACCTTGAGTT 1260
Db 1201 AAGAAATATGAGGAAAAAATTCAGATATCTGGGAGCACTATAAATCACCTTGAGTT 1260
QY 1261 CTGGTTGCAGATCTAGTGAATGCTCAGAAAGACAGTATGCAAGTGAAGTCAAGTCAAGT 1320
Db 1261 CTGGTTGCAGATCTAGTGAATGCTCAGAAAGACAGTATGCAAGTGAAGTCAAGTCAAGT 1320
QY 1321 TCATTACAGAAACAGATTAGTACTGAGACGACCTAAGGCGCTGCAAGAGGAGAGCTT 1380
Db 1321 TCATTACAGAAACAGATTAGTACTGAGACGACCTAAGGCGCTGCAAGAGGAGAGCTT 1380
QY 1381 TGCAAAATCTGTATGGATAGAAATATTGCTATCTGTTTTCCTTGTGGACATCTAGTC 1440
Db 1381 TGCAAAATCTGTATGGATAGAAATATTGCTATCTGTTTTCCTTGTGGACATCTAGTC 1440
QY 1441 ACTGTAAACAATGTGCTGAAGCAGTTGACAAGTGCCTTACACAGTCATTACT 1500
Db 1441 ACTGTAAACAATGTGCTGAAGCAGTTGACAAGTGCCTTACACAGTCATTACT 1500
QY 1501 TTCAAGCAAAAATTTTATGCTCTTAATCTAATCTCTATAGTAGGCATGTTATGTTCT 1560
Db 1501 TTCAAGCAAAAATTTTATGCTCTTAATCTAATCTCTATAGTAGGCATGTTATGTTCT 1560
QY 1561 TATTACCCCTGATTGATGTGATGTGAATGAACTTAACTTAATCAGGATTTGAATTTCCAT 1620
Db 1561 TATTACCCCTGATTGATGTGATGTGAATGAACTTAACTTAATCAGGATTTGAATTTCCAT 1620
QY 1621 TAGCATTTGCTACCAAGTAGGAAAAAATGATACATGGCAGTGTGTTAGTTGGCAATATA 1680
Db 1621 TAGCATTTGCTACCAAGTAGGAAAAAATGATACATGGCAGTGTGTTAGTTGGCAATATA 1680
QY 1681 ATCTTTGAAATTTCTGATTTTTCAGGATATAGCTGTATATCAATTTTTTTTACTGTTA 1740
Db 1681 ATCTTTGAAATTTCTGATTTTTCAGGATATAGCTGTATATCAATTTTTTTTACTGTTA 1740
```

```
QY 1741 TTTAAATGAACCACTAGACTAAGAATAAGAAGCATCATACTATAACTGAACACAATCTGT 1800
Db 1741 TTTAAATGAACCACTAGACTAAGAATAAGAAGCATCATACTATAACTGAACACAATCTGT 1800
QY 1801 ATTCATAGTACTGATTTAAATTTCTAAGTGAAGTGAATTAATCATCTCGATTTTTTAT 1860
Db 1801 ATTCATAGTACTGATTTAAATTTCTAAGTGAAGTGAATTAATCATCTCGATTTTTTAT 1860
QY 1861 TCCTTTTCAGATAGGCTTAACAAATGGAGCTTCTGTATATAAATGTGGAGATTAGAGTTA 1920
Db 1861 TCCTTTTCAGATAGGCTTAACAAATGGAGCTTCTGTATATAAATGTGGAGATTAGAGTTA 1920
QY 1921 ATCTCCCAATCACATAATTTGTTGTTGTAAGGAGTAAATTTCTCCATGCTGCTG 1980
Db 1921 ATCTCCCAATCACATAATTTGTTGTTGTAAGGAGTAAATTTCTCCATGCTGCTG 1980
QY 1981 GAAAGATAGAGATTGTTTTAGAGGTTGGTTGTTGTTTTAGGATTCTCTGCCATTTTCT 2040
Db 1981 GAAAGATAGAGATTGTTTTAGAGGTTGGTTGTTGTTTTAGGATTCTCTGCCATTTTCT 2040
QY 2041 T 2041
Db 2041 T 2041
```

```
RESULT 8
PCT-US02-11758-25
; Sequence 25, Application PC/TUS0211758
; GENERAL INFORMATION:
; APPLICANT: PTC Therapeutics, Inc.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING SMALL MOLECULES THAT BIND SPECIFIC RNA
; FILE OF INVENTION: STRUCTURAL MOTIFS
; FILE REFERENCE: 10589-008-228
; CURRENT APPLICATION NUMBER: PCT/US02/11758
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/282,966
; PRIOR FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-11758-25
```

```
Query Match 38.0%; Score 1990; DB 1; Length 2540;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAAGGTGCACAAGTCCTATTTTCAAGACAAGATGACTTTTAAACAGTTTGAAGGATCT 60
Db 1 GAAAGGTGCACAAGTCCTATTTTCAAGACAAGATGACTTTTAAACAGTTTGAAGGATCT 60
QY 61 AAAAATCTGTACTGTCAGACATCAATAAGGAAGAAGAATTTGTAGAAGAGTTTAATAGA 120
Db 61 AAAAATCTGTACTGTCAGACATCAATAAGGAAGAAGAATTTGTAGAAGAGTTTAATAGA 120
QY 121 TTAACAATCTTTCCTTAATTTTCCAAAGTGTAGTCTGTTTCAGCATCAACACTGGCAGCA 180
Db 121 TTAACAATCTTTCCTTAATTTTCCAAAGTGTAGTCTGTTTCAGCATCAACACTGGCAGCA 180
QY 181 GCAGGGTTCTTTTATCTACTGTTGAAGGAGATACCGTGGGGTCTTTAGTTCTCATGAGCT 240
Db 181 GCAGGGTTCTTTTATCTACTGTTGAAGGAGATACCGTGGGGTCTTTAGTTCTCATGAGCT 240
QY 241 GTAGATAGATGGCAATATGGAGACTCAGCAGTTTGAAGACACAGAAAGATATCCCCAAAT 300
Db 241 GTAGATAGATGGCAATATGGAGACTCAGCAGTTTGAAGACACAGAAAGATATCCCCAAAT 300
QY 301 TGCAGATTTATCAACGGCTTTTATCTTGAATAATAGTGCCACGAGCTACAAAATTTCTGGT 360
Db 301 TGCAGATTTATCAACGGCTTTTATCTTGAATAATAGTGCCACGAGCTACAAAATTTCTGGT 360
```

Qy 361 ATCCAGAAATGCTCAGTACAAAGTTGAAAGTATCTGGGAAGCAGAGATCAATTTTGCCTTA 420  
Db 361 ATCCAGAAATGCTCAGTACAAAGTTGAAAGTATCTGGGAAGCAGAGATCAATTTTGCCTTA 420  
Qy 421 GACAGGCCATCTGAGACACATGCGAGACTATCTTTTGAGAACTGGCAGGTTGTAGATATA 480  
Db 421 GACAGGCCATCTGAGACACATGCGAGACTATCTTTTGAGAACTGGCAGGTTGTAGATATA 480  
Qy 481 TCAGACACCATATATCCCGAGGAACCTGCCATGTATAGTGAAGAGCTAGATTAAGTCC 540  
Db 481 TCAGACACCATATATCCCGAGGAACCTGCCATGTATAGTGAAGAGCTAGATTAAGTCC 540  
Qy 541 TTTCCAGAACTGGCAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTCTGGAGTC 600  
Db 541 TTTCCAGAACTGGCAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTCTGGAGTC 600  
Qy 601 TACTACACAGGTATGTTGACCAAGTGCAGTGCCTTTTGTGTTGGTGGAAACTGAAAT 660  
Db 601 TACTACACAGGTATGTTGACCAAGTGCAGTGCCTTTTGTGTTGGTGGAAACTGAAAT 660  
Qy 661 TGGGAACCTTGTGATCGTGCCTGCTGAGAACACAGGCGACACTTCCCTAAATGCTTCCTT 720  
Db 661 TGGGAACCTTGTGATCGTGCCTGCTGAGAACACAGGCGACACTTCCCTAAATGCTTCCTT 720  
Qy 721 GTTTTGGCCGGAATCTTAATATTGGAAGTGAATCTGATGCTGAGTCTGATAGGAAT 780  
Db 721 GTTTTGGCCGGAATCTTAATATTGGAAGTGAATCTGATGCTGAGTCTGATAGGAAT 780  
Qy 781 TTCCCAATTCACAAATCTTCCCAAGAAATCCATCCATGCGAGATTAAGACGCGGATC 840  
Db 781 TTCCCAATTCACAAATCTTCCCAAGAAATCCATCCATGCGAGATTAAGACGCGGATC 840  
Qy 841 TTTACTTTTGGACATGATATACCTCAGTTAAAGAGGAGCTTGCAGAGCTGGATTT 900  
Db 841 TTTACTTTTGGACATGATATACCTCAGTTAAAGAGGAGCTTGCAGAGCTGGATTT 900  
Qy 901 TATGCTTTAGTGAAGTGAATAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 960  
Db 901 TATGCTTTAGTGAAGTGAATAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 960  
Qy 961 TGGAGCCCATGAGAGCCCTTGGGAACAACATGCTAAATGGTATCCAGGTTGCAATAT 1020  
Db 961 TGGAGCCCATGAGAGCCCTTGGGAACAACATGCTAAATGGTATCCAGGTTGCAATAT 1020  
Qy 1021 CTGTTAGAACAGAGGGAACAAGATATATAACAATATTCATTTAACTCATTCCTTCAG 1080  
Db 1021 CTGTTAGAACAGAGGGAACAAGATATATAACAATATTCATTTAACTCATTCCTTCAG 1080  
Qy 1081 GAGTGTCTGTAAGAACTTACTGAGAAACACCATCCTTAAGTAAAGTAAAGTAAAGTAAAGT 1140  
Db 1081 GAGTGTCTGTAAGAACTTACTGAGAAACACCATCCTTAAGTAAAGTAAAGTAAAGTAAAGT 1140  
Qy 1141 ATCTTCCAAATCTTATGTTACAGAACTATACAAATGAGGTTTCAAGGACAT 1200  
Db 1141 ATCTTCCAAATCTTATGTTACAGAACTATACAAATGAGGTTTCAAGGACAT 1200  
Qy 1201 AAGAAATATGAGGAAATATCAGATATCTGGGACCACTATAAATCACTTCAGTT 1260  
Db 1201 AAGAAATATGAGGAAATATCAGATATCTGGGACCACTATAAATCACTTCAGTT 1260  
Qy 1261 CTGTTGAGATCTAGTGAATGCTCAGAAAGACAGTATGCAAGATGAGTCAAGTCAAGT 1320  
Db 1261 CTGTTGAGATCTAGTGAATGCTCAGAAAGACAGTATGCAAGATGAGTCAAGTCAAGT 1320  
Qy 1321 TCATTACAGAAAGATATTAGTACAGAGAGCTTAAGGCGCTGCAAGAGAGAGCTT 1380  
Db 1321 TCATTACAGAAAGATATTAGTACAGAGAGCTTAAGGCGCTGCAAGAGAGAGCTT 1380  
Qy 1381 TCGAAATCTCTATGATAGAAATATGCTATGCTTTTGTCTTCTGCTGAGCATCTAGTC 1440  
Db 1381 TCGAAATCTCTATGATAGAAATATGCTATGCTTTTGTCTTCTGCTGAGCATCTAGTC 1440

Qy 1441 ACTTGTAAACAATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGTCAATTA 1500  
Db 1441 ACTTGTAAACAATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGTCAATTA 1500  
Qy 1501 TTCAGCAAAAATTTTATGCTTAATCTAACCTATATAGTAGGCACTGTTATGTTGTTCT 1560  
Db 1501 TTCAGCAAAAATTTTATGCTTAATCTAACCTATATAGTAGGCACTGTTATGTTGTTCT 1560  
Qy 1561 TATTACCCCTGATGTAATGTGATGTAAGTCACTTTTAAAGTAAATCAGGATTTGAATTCAT 1620  
Db 1561 TATTACCCCTGATGTAATGTGATGTAAGTCACTTTTAAAGTAAATCAGGATTTGAATTCAT 1620  
Qy 1621 TAGCATTTGCTACCAAGTAGGAAAAAATGTACATGGCAGTGTGTTAGTGGCAATATA 1680  
Db 1621 TAGCATTTGCTACCAAGTAGGAAAAAATGTACATGGCAGTGTGTTAGTGGCAATATA 1680  
Qy 1681 ATCTTTGAATTTCTTGATTTTTCAGGGTATTAGCTGTATATCCATTTTTTACTGTTA 1740  
Db 1681 ATCTTTGAATTTCTTGATTTTTCAGGGTATTAGCTGTATATCCATTTTTTACTGTTA 1740  
Qy 1741 TTTAATTGAAACCATAGACTAAGATAAGAGCATCATCTATAACTGAACAATGTGT 1800  
Db 1741 TTTAATTGAAACCATAGACTAAGATAAGAGCATCATCTATAACTGAACAATGTGT 1800  
Qy 1801 ATTCATAGTATACCTGATTAATTTCTAAGTGTAAAGTGAATTAATCATCTGGATTTTAT 1860  
Db 1801 ATTCATAGTATACCTGATTAATTTCTAAGTGTAAAGTGAATTAATCATCTGGATTTTAT 1860  
Qy 1861 TCTTTTCAGATAGGCTTAACAAATGAGCTTTCTCTATATATAAATGAGATTAAGTTA 1920  
Db 1861 TCTTTTCAGATAGGCTTAACAAATGAGCTTTCTCTATATATAAATGAGATTAAGTTA 1920  
Qy 1921 ATCTCCCCAATCACATAATTTGTTTGTGAAAAAGGAATAAATGTTCCATGCTGGTG 1980  
Db 1921 ATCTCCCCAATCACATAATTTGTTTGTGAAAAAGGAATAAATGTTCCATGCTGGTG 1980  
Qy 1981 GAAAGATAGAGATTTTGTAGAGTGTGTTGTTGTTTGTAGGATTCGTCCATTTTCT 2040  
Db 1981 GAAAGATAGAGATTTTGTAGAGTGTGTTGTTGTTTGTAGGATTCGTCCATTTTCT 2040  
Qy 2041 T 2041  
Db 2041 T 2041

## RESULT 9

US-08-576-956-3  
; Sequence 3, Application US/08576956  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G.  
; APPLICANT: Mackenzie, Alexander E.  
; APPLICANT: Baird, Stephen  
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/576,956  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/511,485

```

: FILING DATE: 04-AUG-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Clark, Paul T.
: REGISTRATION NUMBER: 30,162
: REFERENCE/DOCKET NUMBER: 07891/002001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617/542-5070
: TELEFAX: 617/542-8906
: TELEX: 200154
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2540 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: both
: MOLECULE TYPE: DNA (genomic)
: US-08-576-956-3

```

Query Match 38.0%; Score 1990; DB 9; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2040; Conservative 0; Mismatches 1; Indels 0

QY	1	GA	AAAGTGGACAAGTCTATATTTTCAGAGAAGATGACTTTTAAACAGTTTTGAAGGATCT	60
DB	1	GA	AAAGTGGACAAGTCTATATTTTCAGAGAAGATGACTTTTAAACAGTTTTGAAGGATCT	60
QY	61	AA	AACTTGTGTAACGTGCAGACATCAATPAGGAAGAATAATTGTAGAGAGTTTAAATAGA	120
DB	61	AA	AACTTGTGTAACGTGCAGACATCAATPAGGAAGAAGAATTGTAGAGAGTTTAAATAGA	120
QY	121	TT	AAAAACTTTTGCCTAAATTTTCCAAGTGGPAGTCCGTTCAGCATCAACACTGGCACCA	180
DB	121	TT	AAAAACTTTTGCCTAAATTTTCCAAGTGGPAGTCCGTTCAGCATCAACACTGGCACCA	180
QY	181	GC	AGGGTCTCTTATACTGGTGAAGAGATACCGTGGGTGCTTTAGTTGTTCATGCAGCT	240
DB	181	GC	AGGGTCTCTTATACTGGTGAAGAGATACCGTGGGTGCTTTAGTTGTTCATGCAGCT	240
QY	241	GT	AGATAGATGGCAATATGAGAGACTCAGCAGTTGGGAAGACACAGGAAAGTATCCCCAAAT	300
DB	241	GT	AGATAGATGGCAATATGAGAGACTCAGCAGTTGGGAAGACACAGGAAAGTATCCCCAAAT	300
QY	301	TG	CAGATTTATCAACGGCTTTTATCTTGAATAATAGTGCACCGAGTCTACAAATTCGTGT	360
DB	301	TG	CAGATTTATCAACGGCTTTTATCTTGAATAATAGTGCACCGAGTCTACAAATTCGTGT	360
QY	361	AT	CCAGAATCGTTCAGTACAAAGTTGAAACTATCTCGGAAGCAGAGATCATTTTGCCTTA	420
DB	361	AT	CCAGNATGGTTCAGTACAAAGTTGAAACTATCTCGGAAGCAGAGATCATTTTGCCTTA	420
QY	421	GAC	AGCCATCTGAGACACATGCAGACTATCTTTTGAGAACTGGGCAGGTTGTAGATATA	480
DB	421	GAC	AGCCATCTGAGACACATGCAGACTATCTTTTGAGAACTGGGCAGGTTGTAGATATA	480
QY	481	TC	AGACACATATACCCGAGGAACCTGCCATGTATAGTGAAGAAGCTAGATTAAGTCC	540
DB	481	TC	AGACACCATATACCCGAGGAACCTGCCATGTATAGTGAAGAAGCTAGATTAAGTCC	540
QY	541	TTT	CAGACTGGCCAGACATATGCTCACTTAACCCGAAGAGATTAGCAAGTCTGGAGTTC	600
DB	541	TTT	CAGACTGGCCAGACATATGCTCACTTAACCCGAAGAGATTAGCAAGTCTGGAGTTC	600
QY	601	TACT	TACACAGGTAATGGTGACCAAGTGCAGTGCCTTTGTGTGGTGGAAAACCTGAAAAT	660
DB	601	TACT	TACACAGGTAATGGTGACCAAGTGCAGTGCCTTTGTGTGGTGGAAAACCTGAAAAT	660
QY	661	TGG	GAACCTTGTGATCGTGCCTGGTCAGAACACAGCGGACACTTTCCTAATTTGCTCTTT	720
DB	661	TGG	GAACCTTGTGATCGTGCCTGGTCAGAACACAGCGGACACTTTCCTAATTTGCTCTTT	720
QY	721	GTTT	GGCGGGAATCTTAATATTCGAAGTGAATCTGATGCCTGAGTTCTCATAGGAAT	780

QY 1861 TCTTTTCAGATAGGCTTAACAAATGAGCTTCTCTATATAAATGAGAGATTAGAGTTA 1920  
D 1861 TCTTTTCAGATAGGCTTAACAAATGAGCTTCTCTATATAAATGAGAGATTAGAGTTA 1920  
QY 1921 ATCTCCCAATACATATAATTTGTTTGTGTAAGAAAGAAATGTTCCATGCTGTTG 1980  
D 1921 ATCTCCCAATACATATAATTTGTTTGTGTAAGAAAGAAATGTTCCATGCTGTTG 1980  
QY 1981 GAAAGATAGAGATGCTTTTATAGAGGTTGTTCTGTTTATAGGATCTGTCCTATTTCT 2040  
D 1981 GAAAGATAGAGATGCTTTTATAGAGGTTGTTCTGTTTATAGGATCTGTCCTATTTCT 2040  
QY 2041 T 2041  
D 2041 T 2041

RESULT 10  
US-08-576-956A-3  
; Sequence 3, Application US/08576956A  
; GENERAL INFORMATION:  
; APPLICANT: Korneiuk, Robert G.  
; APPLICANT: Mackenzie, Alexander E.  
; APPLICANT: Baird, Stephen  
; APPLICANT: Liston, Peter  
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Clark & Elbing LLP  
; STREET: 176 Federal Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq Version 2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/576.956A  
; FILING DATE: 22-DEC-95  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/511,485  
; FILING DATE: 04-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 07891/003001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-428-0200  
; TELEFAX: 617-428-7045  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; . SEQUENCE CHARACTERISTICS:  
; LENGTH: 2540 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: DNA (genomic)  
US-08-576-956A-3  
Query Match 38.0%; Score 1990; DB 9; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAAGGTGGACAACTCTATTTTCAAGAGAGATGACTTTTAAACAGTTTGAAGATCT 60  
D 1 GAAAGGTGGACAACTCTATTTTCAAGAGAGATGACTTTTAAACAGTTTGAAGATCT 60

QY 61 AAAAATCTGTACCTGCAGACATCAATAGGAAGAAATTTGTAGAGAGTTTAAATAGA 120  
D 61 AAAAATCTGTACCTGCAGACATCAATAGGAAGAAATTTGTAGAGAGTTTAAATAGA 120  
QY 121 TTAATAATCTTTGCTTAATTTTCCAAAGTGGTAGTCTCTGTTTCAGCATCAACACTGGCACA 180  
D 121 TTAATAATCTTTGCTTAATTTTCCAAAGTGGTAGTCTCTGTTTCAGCATCAACACTGGCACA 180  
QY 181 GCAGGTTTCTTTTACTGGTGAAGAGATACCGTGGGTGCTTTAGTTGTCTATGACGCT 240  
D 181 GCAGGTTTCTTTTACTGGTGAAGAGATACCGTGGGTGCTTTAGTTGTCTATGACGCT 240  
QY 241 GTAGATAGATGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAAGATATCCCAAAAT 300  
D 241 GTAGATAGATGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAAGATATCCCAAAAT 300  
QY 301 TGCAGATTTATCAACGGCTTTTATCTTGAATAATAGTGGCCACGAGTCTACAAATTTCTGCT 360  
D 301 TGCAGATTTATCAACGGCTTTTATCTTGAATAATAGTGGCCACGAGTCTACAAATTTCTGCT 360  
QY 361 ATCCAGAAATGGTCACTACAAAGTTGAAAGTATCTGGGAAGCAGAGATCATTTTGCCTTA 420  
D 361 ATCCAGAAATGGTCACTACAAAGTTGAAAGTATCTGGGAAGCAGAGATCATTTTGCCTTA 420  
QY 421 GACAGGCCATCTGAGACACATGCAGACTATCTTTTGAAGAACTGGCAGGTTGTAGATATA 480  
D 421 GACAGGCCATCTGAGACACATGCAGACTATCTTTTGAAGAACTGGCAGGTTGTAGATATA 480  
QY 481 TCAGACACATATACCCGAGGAAACCTGCGCATGTATGTGAAGAGCTAGATTAAGTCC 540  
D 481 TCAGACACATATACCCGAGGAAACCTGCGCATGTATGTGAAGAGCTAGATTAAGTCC 540  
QY 541 TTTTCAGAACTGGCCAGACTATCTCACCTAACCCCAAGAGAGTTAGCAAGTCTGGACTC 600  
D 541 TTTTCAGAACTGGCCAGACTATCTCACCTAACCCCAAGAGAGTTAGCAAGTCTGGACTC 600  
QY 601 TACTACACAGTATTTGGTCAACCAAGTGCAGTCTTTTGTGGTGGAAAGTCTGAAAT 660  
D 601 TACTACACAGTATTTGGTCAACCAAGTGCAGTCTTTTGTGGTGGAAAGTCTGAAAT 660  
QY 661 TGGGAACCTTGTGATCGTGGCTGTCAGAACACAGCGGACACTTTTCTTAATTTGCTCTTT 720  
D 661 TGGGAACCTTGTGATCGTGGCTGTCAGAACACAGCGGACACTTTTCTTAATTTGCTCTTT 720  
QY 721 GTTTTGGGCGGAATCTTAATATTCGAACTGAATCTGTGCTGTGATGAGAT 780  
D 721 GTTTTGGGCGGAATCTTAATATTCGAACTGAATCTGTGCTGTGATGAGAT 780  
QY 781 TTCCCAAAATTCACAAATCTTCCAAAGAAATCCATCCATGGCAGATTATGAAGCAGGATC 840  
D 781 TTCCCAAAATTCACAAATCTTCCAAAGAAATCCATCCATGGCAGATTATGAAGCAGGATC 840  
QY 841 TTTTACTTTTGGGACATGGATATACCTAGTTAACAGGAGCAGCTTTCAGAGAGCTGGATTT 900  
D 841 TTTTACTTTTGGGACATGGATATACCTAGTTAACAGGAGCAGCTTTCAGAGAGCTGGATTT 900  
QY 901 TATGCTTTAGGTGAAGGTGATTAAGTCTTTTCACTGTGGAGGCGCTAACTGAT 960  
D 901 TATGCTTTAGGTGAAGGTGATTAAGTCTTTTCACTGTGGAGGCGCTAACTGAT 960  
QY 961 TGGAAAGCCAGTGAAGACCTTTGGGAACAAATGCTAAATGGTATCCAGGGTGCATAAT 1020  
D 961 TGGAAAGCCAGTGAAGACCTTTGGGAACAAATGCTAAATGGTATCCAGGGTGCATAAT 1020  
QY 1021 CTGTTTAGAACAGAGGACAAATATATAAACAATATTTCACTTAATTAATTAATTAATTAAT 1080  
D 1021 CTGTTTAGAACAGAGGACAAATATATAAACAATATTTCACTTAATTAATTAATTAATTAAT 1080  
QY 1081 GAGTGTCTGGTGAAGTACTACTGAGAAACACCATCACTAAGTAAAGATTTGATGATAC 1140  
D 1081 GAGTGTCTGGTGAAGTACTACTGAGAAACACCATCACTAAGTAAAGATTTGATGATAC 1140  
QY 1141 ATCTTCCAAATCTCTATGTTTACAAAGAGCTATACGAATGGGTTTCAAGGAGATTT 1200



```
Db 1141 ATCTTCAAAATCCTATGGTACAGAGCTATACGAAATGGGTTCAGTTTCAAGGACATT 1200
QY 1201 AAGAAATATAGGAGGAAAAATTCAGATATCTGGGAGCAACTATAAATCAGTTGAGGTT 1260
Db 1201 AAGAAATATAGGAGGAAAAATTCAGATATCTGGGAGCAACTATAAATCAGTTGAGGTT 1260
QY 1261 CTGGTTCAGATCTAGTGAATGCTCAGAAAGACAGATATGCAAGATGAGTCAAGTCAGACT 1320
Db 1261 CTGGTTCAGATCTAGTGAATGCTCAGAAAGACAGATATGCAAGATGAGTCAAGTCAGACT 1320
QY 1321 TCATTACAGAAACAGATAGTACTGAGAGCAGCTAAGGCGCTGCAAGAGGAGAGCTT 1380
Db 1321 TCATTACAGAAACAGATAGTACTGAGAGCAGCTAAGGCGCTGCAAGAGGAGAGCTT 1380
QY 1381 TGCAAAATCTGTATGGATAGAAAATATGCTATCTGTTTCTCTTCTGTTGACATCTAGTC 1440
Db 1381 TGCAAAATCTGTATGGATAGAAAATATGCTATCTGTTTCTCTTCTGTTGACATCTAGTC 1440
QY 1441 ACTTGTAACAATGTGCTGAAGCAGTTGACAAGTGCCCAATGTGCTACACAGTCATTACT 1500
Db 1441 ACTTGTAACAATGTGCTGAAGCAGTTGACAAGTGCCCAATGTGCTACACAGTCATTACT 1500
QY 1501 TTCAAGCAAAAATTTTATGCTCTTAATCTAACTCTATAGTAGGCATGTTATGTTCTT 1560
Db 1501 TTCAAGCAAAAATTTTATGCTCTTAATCTAACTCTATAGTAGGCATGTTATGTTCTT 1560
QY 1561 TATTACCTGATTGAATGTGTGATGTGAAGTGAATTAAGTAACTCAGGATTAATGCCAT 1620
Db 1561 TATTACCTGATTGAATGTGTGATGTGAAGTGAATTAAGTAACTCAGGATTAATGCCAT 1620
QY 1621 TAGCATTGCTACCAAGTAGGAAAAAATGTACATGGCAGTCTTTTAGTTGGCAATATA 1680
Db 1621 TAGCATTGCTACCAAGTAGGAAAAAATGTACATGGCAGTCTTTTAGTTGGCAATATA 1680
QY 1681 ATCTTTGAATTTCTGATTTTTCAGGGTATTAGCTGTATATCCATTTTTTACTGTTA 1740
Db 1681 ATCTTTGAATTTCTGATTTTTCAGGGTATTAGCTGTATATCCATTTTTTACTGTTA 1740
QY 1741 TTTTAATGAAACCATAGACTAAGAATAAAGACATCATACTATACTGAACACAATGTGT 1800
Db 1741 TTTTAATGAAACCATAGACTAAGAATAAAGACATCATACTATACTGAACACAATGTGT 1800
QY 1801 ATTCATAGTATAGTAAATTTCTAAGTGTAAAGTCAATTAATCATCTGGATTTTTAT 1860
Db 1801 ATTCATAGTATAGTAAATTTCTAAGTGTAAAGTCAATTAATCATCTGGATTTTTAT 1860
QY 1861 TCCTTTTCAGATAGGCTTAACAATGGAGCTTCTGTATATAAATGTGGAGATTAGAGTTA 1920
Db 1861 TCCTTTTCAGATAGGCTTAACAATGGAGCTTCTGTATATAAATGTGGAGATTAGAGTTA 1920
QY 1921 ATCTCCCAATCACATAATTTGTTTGTGTAAGAAAGGAATAAATGTTCCATGCTGGTG 1980
Db 1921 ATCTCCCAATCACATAATTTGTTTGTGTAAGAAAGGAATAAATGTTCCATGCTGGTG 1980
QY 1981 GAAAGATAGAGATGTTTTAGAGTTGGTGTGTTGTTTTAGGATTCGTCCATTTCT 2040
Db 1981 GAAAGATAGAGATGTTTTAGAGTTGGTGTGTTGTTTTAGGATTCGTCCATTTCT 2040
QY 2041 T 2041
Db 2041 T 2041
```

RESULT 11  
US-09-011-356-3  
; Sequence 3, Application US/09011356  
; GENERAL INFORMATION:  
; APPLICANT: Korneluz, Robert G.  
; APPLICANT: Mackenzie, Alexander E.  
; APPLICANT: Baird, Stephen  
; APPLICANT: Liston, Peter  
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,

; TITLE OF INVENTION: PROBES, AND DETECTION METHODS  
; FILE REFERENCE: 07891/003002  
; CURRENT APPLICATION NUMBER: US/09/011,356  
; EARLIER FILING DATE: 1998-09-14  
; EARLIER APPLICATION NUMBER: PCT/IB96/01022  
; EARLIER FILING DATE: 1996-08-05  
; EARLIER APPLICATION NUMBER: 08/576,956  
; EARLIER FILING DATE: 1995-12-22  
; EARLIER APPLICATION NUMBER: 08/511,485  
; EARLIER FILING DATE: 1995-08-04  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 2540  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: variation  
; LOCATION: (2540)...(2540)  
; OTHER INFORMATION: N may be any nucleotide  
US-09-011-356-3

Query Match 38.0%; Score 1990; DB 14; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GAAAGGTGACAAAGTCCTATTTTCAAGAGAAGATGACTTTTAAACAGTTTTGAAGGATCT 60  
Db 1 GAAAGGTGACAAAGTCCTATTTTCAAGAGAAGATGACTTTTAAACAGTTTTGAAGGATCT 60  
QY 61 AAAACCTTGTTGTAACATCAATTAAGGAAGAAGAATTTGTAGAAGAGTTTAAATAGA 120  
Db 61 AAAACCTTGTTGTAACATCAATTAAGGAAGAAGAATTTGTAGAAGAGTTTAAATAGA 120  
QY 121 TTAATAACCTTTTCTTAATTTTCAAGTGGTAGTCCCTGTTTTCAGCATCAACACTGGCACA 180  
Db 121 TTAATAACCTTTTCTTAATTTTCAAGTGGTAGTCCCTGTTTTCAGCATCAACACTGGCACA 180  
QY 181 GCAGGTTTCTTATACTGTTGAAGGAGATACCGTGGGTGCTTTAGTTTCTCATGCGAGCT 240  
Db 181 GCAGGTTTCTTATACTGTTGAAGGAGATACCGTGGGTGCTTTAGTTTCTCATGCGAGCT 240  
QY 241 GTAGATAGATGGCAATATGGAGACTCAGCAGTTGGGAAGACACAGGAAGATATCCCCAAAT 300  
Db 241 GTAGATAGATGGCAATATGGAGACTCAGCAGTTGGGAAGACACAGGAAGATATCCCCAAAT 300  
QY 301 TGCAGATTTATCAACGGCTTTTATCTTGAATAAGTAGTCCACGCGAGTCAACAATCTGGT 360  
Db 301 TGCAGATTTATCAACGGCTTTTATCTTGAATAAGTAGTCCACGCGAGTCAACAATCTGGT 360  
QY 361 ATCCAGAATGGTCAGTACAAAAGTTGAAAACATATCTGGGAAGCAGAGATCATTTTGGCTTA 420  
Db 361 ATCCAGAATGGTCAGTACAAAAGTTGAAAACATATCTGGGAAGCAGAGATCATTTTGGCTTA 420  
QY 421 GACAGGCCATCTGAGACACATGCAAGTATCTTTTGAAGAACTGGGCGAGTTGTAGATATA 480  
Db 421 GACAGGCCATCTGAGACACATGCAAGTATCTTTTGAAGAACTGGGCGAGTTGTAGATATA 480  
QY 481 TCAGACACCATATATACCGGAGAACCTGCCATCTATAGTGAACAAGCTAGATTAAAGTCC 540  
Db 481 TCAGACACCATATATACCGGAGAACCTGCCATCTATAGTGAACAAGCTAGATTAAAGTCC 540  
QY 541 TTTTCAGAACTGGCGAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTCTGGACTC 600  
Db 541 TTTTCAGAACTGGCGAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTCTGGACTC 600  
QY 601 TACTACACAGGTTATGGTGACCAAGTGCAGTCTTTTGTGTGGTGAAGAACTGAAAAAT 660  
Db 601 TACTACACAGGTTATGGTGACCAAGTGCAGTCTTTTGTGTGGTGAAGAACTGAAAAAT 660  
QY 661 TGGGAACCTTGTGATCTGCTGCTCAGAACACAGCGGACACTTTCTTAATTTCTTCTTT 720  
Db 661 TGGGAACCTTGTGATCTGCTGCTCAGAACACAGCGGACACTTTCTTAATTTCTTCTTT 720



```
QY 721 GTTTGGCCGGAATCTTAATATTCGAAGTAATCTGATGCTGAGTCTCGATAGGAAT 780
DB 721 GTTTGGCCGGAATCTTAATATTCGAAGTAATCTGATGCTGAGTCTCGATAGGAAT 780
QY 781 TTCCCAAAATCAACAAATCTTCCCAAGAAATCCATCCATGGCAGATTAATGAAGCAGGATC 840
DB 781 TTCCCAAAATCAACAAATCTTCCCAAGAAATCCATCCATGGCAGATTAATGAAGCAGGATC 840
QY 841 TTTACTTTTGGGACATGATATACCTACGTTACAAAGGAGCAGCTTGCAGAGCTGGATTT 900
DB 841 TTTACTTTTGGGACATGATATACCTACGTTACAAAGGAGCAGCTTGCAGAGCTGGATTT 900
QY 901 TATGCTTTTAGGTGAAGGTGATAAGCTAAAGTCTTTCACCTGTGGAGGAGGGCTAACTGAT 960
DB 901 TATGCTTTTAGGTGAAGGTGATAAGCTAAAGTCTTTCACCTGTGGAGGAGGGCTAACTGAT 960
QY 961 TGGAAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCAAAATAT 1020
DB 961 TGGAAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCAAAATAT 1020
QY 1021 CTGTTAGAACAGAGGACAGAAATATATAACAATATTCATTTAACTCATTCCTTGAG 1080
DB 1021 CTGTTAGAACAGAGGACAGAAATATATAACAATATTCATTTAACTCATTCCTTGAG 1080
QY 1081 GAGTGTCTGTTAAGAACTACTGAGAAACACCATCACTAACTAGAGAATTTGATGATACC 1140
DB 1081 GAGTGTCTGTTAAGAACTACTGAGAAACACCATCACTAACTAGAGAATTTGATGATACC 1140
QY 1141 ATCTTCCAAAATCCCTATGTTACAGAAGCTATACGAATGGGGTTCAGTTTCAAGGACAT 1200
DB 1141 ATCTTCCAAAATCCCTATGTTACAGAAGCTATACGAATGGGGTTCAGTTTCAAGGACAT 1200
QY 1201 AAGAAATTAATGGAGGAAAAATTCAGATATCTGGGAGCACTATAAATCACTTCAGGTT 1260
DB 1201 AAGAAATTAATGGAGGAAAAATTCAGATATCTGGGAGCACTATAAATCACTTCAGGTT 1260
QY 1261 CTGGTTGACAGATCTAGTGAATGCTCAGAAAGACATATGCAAGATGAGTCAAGTCAAGCT 1320
DB 1261 CTGGTTGACAGATCTAGTGAATGCTCAGAAAGACATATGCAAGATGAGTCAAGTCAAGCT 1320
QY 1321 TCATTACAGAAAGATAGTACTGAAGAGCAGCTAAGGCGCCTCAAGAGGAGAGCTT 1380
DB 1321 TCATTACAGAAAGATAGTACTGAAGAGCAGCTAAGGCGCCTCAAGAGGAGAGCTT 1380
QY 1381 TCCAAATCTGTATGGATAGAAATATGCTATCGTTTTTGTCTTGTGGACATCTAGTC 1440
DB 1381 TCCAAATCTGTATGGATAGAAATATGCTATCGTTTTTGTCTTGTGGACATCTAGTC 1440
QY 1441 ACTTGTAAACAATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGCTCATCT 1500
DB 1441 ACTTGTAAACAATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGCTCATCT 1500
QY 1501 TTCAGCAAAAATTTTATGCTTTAATCTAATCTATAGTAGGAGATGTTATGTTGTCT 1560
DB 1501 TTCAGCAAAAATTTTATGCTTTAATCTAATCTATAGTAGGAGATGTTATGTTGTCT 1560
QY 1561 TATTACCTGATTTGAATGTGATGTGATGTGACTGACCTTTAGTAAATCAGGATTCAAATCCAT 1620
DB 1561 TATTACCTGATTTGAATGTGATGTGATGTGACTGACCTTTAGTAAATCAGGATTCAAATCCAT 1620
QY 1621 TAGCAATTTGCTACCAAGTAGGAAAAAATGACATGGCAGTGTGTTTGTGGCAATATA 1680
DB 1621 TAGCAATTTGCTACCAAGTAGGAAAAAATGACATGGCAGTGTGTTTGTGGCAATATA 1680
QY 1681 ATCTTTGAATTTCTTTGATTTTTCAGGGTATTAGCTGTATATPCCATTTTTTTTACTGTTA 1740
DB 1681 ATCTTTGAATTTCTTTGATTTTTCAGGGTATTAGCTGTATATPCCATTTTTTTTACTGTTA 1740
QY 1741 TTTAATTTGAACCATAGACTAAGATATAGAACATCATCTATTAATCTGAACACAATGTGT 1800
DB 1741 TTTAATTTGAACCATAGACTAAGATATAGAACATCATCTATTAATCTGAACACAATGTGT 1800
```

```
QY 1801 ATTCATAGTACTGATTTAATTTCTAAGTGTAAAGTAATTAATCATCTGGATTTTTTAT 1860
DB 1801 ATTCATAGTACTGATTTAATTTCTAAGTGTAAAGTAATTAATCATCTGGATTTTTTAT 1860
QY 1861 TCTTTTTCAGATAGGCTTAAACAAATGGAGCTTCTGTATATAAATGTGGAGATTAGAGTTA 1920
DB 1861 TCTTTTTCAGATAGGCTTAAACAAATGGAGCTTCTGTATATAAATGTGGAGATTAGAGTTA 1920
QY 1921 ATCTCCCCCAATCACATAATTTCTGTTGTAAGGAAGGAATAAATGTTCCATGCTGGTG 1980
DB 1921 ATCTCCCCCAATCACATAATTTCTGTTGTAAGGAAGGAATAAATGTTCCATGCTGGTG 1980
QY 1981 GAAAGATAGAGATTTTGTAGAGTGTGTTGTTTGTAGGATTCGTGCAATTTTCT 2040
DB 1981 GAAAGATAGAGATTTTGTAGAGTGTGTTGTTTGTAGGATTCGTGCAATTTTCT 2040
QY 2041 T 2041
DB 2041 T 2041

RESULT 12
US-09-011-356-3
; Sequence 3, Application US/09011356A
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003002
; CURRENT APPLICATION NUMBER: US/09/011,356A
; EARLIER FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2540)...(2540)
; OTHER INFORMATION: N may be any nucleotide
US-09-011-356-3

Query Match 38.0%; Score 1990; DB 14; Length 2540;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAAAGGTGGACAAGTCCCTATTTTCAAGAGAGAAGATGACATTTTAAACAGTTTTTGAAGATCT 60
DB 1 GAAAAGGTGGACAAGTCCCTATTTTCAAGAGAGAAGATGACATTTTAAACAGTTTTTGAAGATCT 60
QY 61 AAAACTGTGTACCTGCAGACATCAATAAGGAAGAGAAATTTGTAGAAGAGTTTAATAGA 120
DB 61 AAAACTGTGTACCTGCAGACATCAATAAGGAAGAGAAATTTGTAGAAGAGTTTAATAGA 120
QY 121 TTAATAACTTTTGTCTAAATTTTCCAGTGTGTAGTCTGTTTTCAGCATCAACACTGGCAGCA 180
DB 121 TTAATAACTTTTGTCTAAATTTTCCAGTGTGTAGTCTGTTTTCAGCATCAACACTGGCAGCA 180
QY 181 GCAGGGTTTCTTTATCTACTGTTGAGGAGATACCGTCGGTGTCTTTAGTTGTCTATGAGCT 240
DB 181 GCAGGGTTTCTTTATCTACTGTTGAGGAGATACCGTCGGTGTCTTTAGTTGTCTATGAGCT 240
QY 241 GTAGATAGATGCAATATGGAGACTCAGCAGTTTGGAGACACAGGAAAGTATCCCCCAAT 300
```

```

|||||
Db 241 GTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAGACACAGGAAGTATCCCAAAAT 300
QY TGCAGATTTATCAACGGCTTTTATCTTTGAAAATAGTGCACCGCAGTCTACAAAATTTCTGGT 360
Db TGCAGATTTATCAACGGCTTTTATCTTTGAAAATAGTGCACCGCAGTCTACAAAATTTCTGGT 360
QY ATCCAGAAATGGTCACTACAAAGTTGAAAATCTATCTGGGAAGCAGAGATCATTTTGGCTTTA 420
Db ATCCAGAAATGGTCACTACAAAGTTGAAAATCTATCTGGGAAGCAGAGATCATTTTGGCTTTA 420
QY GACAGGCCATCTCAGACACATGACAGACTATCTTTTGAGAACTGGGAGGTTGAGATATA 480
Db GACAGGCCATCTCAGACACATGACAGACTATCTTTTGAGAACTGGGAGGTTGAGATATA 480
QY TCAGACACCATATATACCCGAGGAACCTGCCATCTATAGTGAAGAAGCTAGATTAAGTCC 540
Db TCAGACACCATATATACCCGAGGAACCTGCCATCTATAGTGAAGAAGCTAGATTAAGTCC 540
QY TTTTCAGAACTGGCCAGACTATGCTCACTAACCCCAAGAGAGTTAGCAAGTGGTGGACTC 600
Db TTTTCAGAACTGGCCAGACTATGCTCACTAACCCCAAGAGAGTTAGCAAGTGGTGGACTC 600
QY TACTACACAGGTATTTGGTGACCAAGTGCAGTGTCTTTTGGTGCGTGAAGAACTGAAAAT 660
Db TACTACACAGGTATTTGGTGACCAAGTGCAGTGTCTTTTGGTGCGTGAAGAACTGAAAAT 660
QY TGGGAACCTTGTGATCGTGGCTGGTGAGAACGAGACACTTTTCTTAATTCCTTCTTT 720
Db TGGGAACCTTGTGATCGTGGCTGGTGAGAACGAGACACTTTTCTTAATTCCTTCTTT 720
QY GTTTTGGGCGGAATCTTAATATTCGAAGTGAATCTGATGCTGTGATGAAGAAAT 780
Db GTTTTGGGCGGAATCTTAATATTCGAAGTGAATCTGATGCTGTGATGAAGAAAT 780
QY TTCCCAAAATTCACAAATCTTCCAGAAATCCATCCATGCGCAGATTAAGACACGAGTAC 840
Db TTCCCAAAATTCACAAATCTTCCAGAAATCCATCCATGCGCAGATTAAGACACGAGTAC 840
QY TTTTACTTTTGGGACATGGATATATCACTTAACAAGGAGCAGCTTGCAGAGCTGGATTT 900
Db TTTTACTTTTGGGACATGGATATATCACTTAACAAGGAGCAGCTTGCAGAGCTGGATTT 900
QY TATGCTTTTAGTGAAGTGATAAAGTAAAGTGTCTTTTCTACTGTGAGAGGGCTTAACCTGAT 960
Db TATGCTTTTAGTGAAGTGATAAAGTAAAGTGTCTTTTCTACTGTGAGAGGGCTTAACCTGAT 960
QY TGGAGCCCACTGAAGCCCTTGGGAACACATGCTAAATGGTATCCAGGGTCCAATAT 1020
Db TGGAGCCCACTGAAGCCCTTGGGAACACATGCTAAATGGTATCCAGGGTCCAATAT 1020
QY CTGTTAGACAGAGGAGCAAGAAATATATAACAATATTCATTTAACTCATTCACCTTGAG 1080
Db CTGTTAGACAGAGGAGCAAGAAATATATAACAATATTCATTTAACTCATTCACCTTGAG 1080
QY GAGTGTCTGGTGAAGAACTACTGAGAAACACCCATCACTAACTAGAAGAAATGATGATACC 1140
Db GAGTGTCTGGTGAAGAACTACTGAGAAACACCCATCACTAACTAGAAGAAATGATGATACC 1140
QY ATCTTCCAAAATCCTATGGTACAGAAAGCTATACGAATGGGTTTCAGTTTCAAGGACAT 1200
Db ATCTTCCAAAATCCTATGGTACAGAAAGCTATACGAATGGGTTTCAGTTTCAAGGACAT 1200
QY AAGAAAATATGAGGAAAAAATTCAGATATCTGGGAGCAACTATAAATCAGCTTGAAGTT 1260
Db AAGAAAATATGAGGAAAAAATTCAGATATCTGGGAGCAACTATAAATCAGCTTGAAGTT 1260
QY CTGGTTGCAGATCTAGTGAATGCTCAGAAAGCAGTATGCAAGATCAGTCAAGTCAGACT 1320
Db CTGGTTGCAGATCTAGTGAATGCTCAGAAAGCAGTATGCAAGATCAGTCAAGTCAGACT 1320
QY TCATTACAGAAAGATTTAGTACTGAAGACGAGCTAAGGGCTGCAAGAGGAGAGCTT 1380
|||||
```

```

Db 1321 TCATTACAGAAAGAGATTAGTACTGAAGACCACTAAGGCCCTGCAAGAGGAGAGCTT 1380
QY TGCAAAATCTGTATGGATAGAAAATATTGCTATATCGTTTTTTTCTTCTTGACATCTAGTC 1440
Db TGCAAAATCTGTATGGATAGAAAATATTGCTATATCGTTTTTTTCTTCTTGACATCTAGTC 1440
QY ACTTGTAAACAATGTGCTGAAGCAGTTGACAAGTGCCTACAGTCACTACT 1500
Db ACTTGTAAACAATGTGCTGAAGCAGTTGACAAGTGCCTACAGTCACTACT 1500
QY TTCAAGCAAAAATTTTTTATGCTCTTAATCTAATCTATAGTAGGCATGTTATGTTCT 1560
Db TTCAAGCAAAAATTTTTTATGCTCTTAATCTAATCTATAGTAGGCATGTTATGTTCT 1560
QY TATTACCCCTGATTGAATGTGATGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1620
Db TATTACCCCTGATTGAATGTGATGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1620
QY TAGCATTTGCTACCAAGTAGGAAAAAATGTACATGGCAGTGTGTTAGTTGGCAATATA 1680
Db TAGCATTTGCTACCAAGTAGGAAAAAATGTACATGGCAGTGTGTTAGTTGGCAATATA 1680
QY ATCTTTGAAATTTCTTGAATTTTTCAGGGTATAGCTGTATATATCCATTTTTTACTGTTA 1740
Db ATCTTTGAAATTTCTTGAATTTTTCAGGGTATAGCTGTATATATCCATTTTTTACTGTTA 1740
QY TTTTAAATGAAACCATAGACTAAGAAATGAAGACATCATATACATGAACAAATGTGT 1800
Db TTTTAAATGAAACCATAGACTAAGAAATGAAGACATCATATACATGAACAAATGTGT 1800
QY ATTCATAGTATACTGATTTAAATTTCTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1860
Db ATTCATAGTATACTGATTTAAATTTCTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1860
QY TCTTTTCAGATAGGCTTAACAAATGGAGCTTTCTGTATATATAAATGTGGAGATTAGAGTTA 1920
Db TCTTTTCAGATAGGCTTAACAAATGGAGCTTTCTGTATATATAAATGTGGAGATTAGAGTTA 1920
QY ATCTCCCAATACATAAATTTGTTTGTGAAAAAGGAAATAAATTTCCATGCTGGTG 1980
Db ATCTCCCAATACATAAATTTGTTTGTGAAAAAGGAAATAAATTTCCATGCTGGTG 1980
QY GAAAGATAGAGATTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 2040
Db GAAAGATAGAGATTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 2040
QY 2041 T 2041
Db 2041 T 2041
```

```

RESULT 13
US-09-023-655-900
: Sequence 900, Application US/09023655
: GENERAL INFORMATION:
: APPLICANT: Cocks, Benjamin G.
: APPLICANT: Susan G. Stuart
: APPLICANT: Jeffrey J. Seilhamer
: TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
: TITLE OF INVENTION: EXPRESSION
: NUMBER OF SEQUENCES: 1508
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
: STREET: 3174 PORTER DRIVE
: CITY: PALO ALTO
: STATE: CALIFORNIA
: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: IBM PC compatible
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
```

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023.655  
FILING DATE: HEREWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0001 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 900:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2540 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: g1184319  
US-09-023-655-900

Query Match 38.0%; Score 1990; DB 14; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	GAAGAGTGGCAAGTCTCTATTTCAGAGAGAGATGACTTTTAACAGTCTTTGAAGGATCT	60
DB	1	GAAGAGTGGCAAGTCTCTATTTCAGAGAGAGATGACTTTTAACAGTCTTTGAAGGATCT	60
QY	61	AAACTGTGTACCTGCAGACATCAATAGGAAGAAATTTGTAGAGAGTTTAATAGA	120
DB	61	AAACTGTGTACCTGCAGACATCAATAGGAAGAAATTTGTAGAGAGTTTAATAGA	120
QY	121	TTAAAACTTTTGTCTAAATTTTCCAAAGTGTAGTCTCTGTTTCAGCATCAACACTGGCACA	180
DB	121	TTAAAACTTTTGTCTAAATTTTCCAAAGTGTAGTCTCTGTTTCAGCATCAACACTGGCACA	180
QY	181	GCAGGTTTCTTTATCTGGTGAAGAGATACCGTGGGTGCTTTAGTTGTCTATGCAGCT	240
DB	181	GCAGGTTTCTTTATCTGGTGAAGAGATACCGTGGGTGCTTTAGTTGTCTATGCAGCT	240
QY	241	GTAGATAGATGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAAGTATCCCAAT	300
DB	241	GTAGATAGATGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAAGTATCCCAAT	300
QY	301	TGCAGATTATCAACGGCTTTTATCTTGAANAATAGTGCACCGCAGTCTACAAATTTCTGGT	360
DB	301	TGCAGATTATCAACGGCTTTTATCTTGAANAATAGTGCACCGCAGTCTACAAATTTCTGGT	360
QY	361	ATCCAGATGGTCACTACAAAGTTGAAACTATCTGGGAAGCAGAGATCATTTTGCCTTA	420
DB	361	ATCCAGATGGTCACTACAAAGTTGAAACTATCTGGGAAGCAGAGATCATTTTGCCTTA	420
QY	421	GACAGCCATCTGAGACACATCAGACTATCTTTTGAAGTGGCAGGTTGTAGATATA	480
DB	421	GACAGCCATCTGAGACACATCAGACTATCTTTTGAAGTGGCAGGTTGTAGATATA	480
QY	481	TCAGACACATATACCGAGGAACCGTGCATCTGATATAGTGAAGAGCTAGATTAAGTCC	540
DB	481	TCAGACACATATACCGAGGAACCGTGCATCTGATATAGTGAAGAGCTAGATTAAGTCC	540
QY	541	TTTCAGAACTGSCAGACTATCTCACCTAACCCCAAGAGGTTAGCAGTCTGCAGCTC	600
DB	541	TTTCAGAACTGSCAGACTATCTCACCTAACCCCAAGAGGTTAGCAGTCTGCAGCTC	600
QY	601	TACTACAGGTTATGGTGACCAAGTGCAGTCTTTTGTGGTGGAAAACTGAAAAAT	660
DB	601	TACTACAGGTTATGGTGACCAAGTGCAGTCTTTTGTGGTGGAAAACTGAAAAAT	660

QY	661	TGGGAACCTTGTGATCGTGCCTGGTCAGAACACAGCGACACTTTCCTAATTCCTTTT	720
DB	661	TGGGAACCTTGTGATCGTGCCTGGTCAGAACACAGCGACACTTTCCTAATTCCTTTT	720
QY	721	GTTTTGGGCGGAATCTTAATATTCGAAGTGAATCTGATGCTGTGAGTTCTGATAGAA	780
DB	721	GTTTTGGGCGGAATCTTAATATTCGAAGTGAATCTGATGCTGTGAGTTCTGATAGAA	780
QY	781	TTCCCAAAATTCACAAATCTTCCAGAAATCCATCCATGGCAGATTTATGAAGCAGGATC	840
DB	781	TTCCCAAAATTCACAAATCTTCCAGAAATCCATCCATGGCAGATTTATGAAGCAGGATC	840
QY	841	TTTACTTTTGGGACATGGATATACCTCAGTTAAAGGAGCAGCTTCAAGAGCTGGATTT	900
DB	841	TTTACTTTTGGGACATGGATATACCTCAGTTAAAGGAGCAGCTTCAAGAGCTGGATTT	900
QY	901	TATGCTTTAGGTGAAGTGAATAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA	960
DB	901	TATGCTTTAGGTGAAGTGAATAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA	960
QY	961	TGGAAGCCCAAGTGAAGACCCCTTGGGAACAACATGCTAAATGTTATCCAGGGTGC	1020
DB	961	TGGAAGCCCAAGTGAAGACCCCTTGGGAACAACATGCTAAATGTTATCCAGGGTGC	1020
QY	1021	CTGTTTAGAACAGAGGACAGAAATATATAAACAATATTCATTTAACCTCATTGAG	1080
DB	1021	CTGTTTAGAACAGAGGACAGAAATATATAAACAATATTCATTTAACCTCATTGAG	1080
QY	1081	GAGTGTCTGGTGAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT	1140
DB	1081	GAGTGTCTGGTGAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT	1140
QY	1141	ATCTTCCAAATTCCTATGTTACAAAGATATACGATGGGTTTCAAGTTCAGGACAT	1200
DB	1141	ATCTTCCAAATTCCTATGTTACAAAGATATACGATGGGTTTCAAGTTCAGGACAT	1200
QY	1201	AAGAAATTAATCGAGGAAAAATTCAGATATCTGGGAGCAACTATATAATCACTT	1260
DB	1201	AAGAAATTAATCGAGGAAAAATTCAGATATCTGGGAGCAACTATATAATCACTT	1260
QY	1261	CTGTTTGCAGATCTAGTGAATGCTCAGAAAGACACTATGCAAGTGAAGTCAAGT	1320
DB	1261	CTGTTTGCAGATCTAGTGAATGCTCAGAAAGACACTATGCAAGTGAAGTCAAGT	1320
QY	1321	TCATTACAGAAAGAGATTTAGTACTGAAAGAGCAGCTAAGGCGCTGCAAGAGGAG	1380
DB	1321	TCATTACAGAAAGAGATTTAGTACTGAAAGAGCAGCTAAGGCGCTGCAAGAGGAG	1380
QY	1381	TGCAAAATCTGTATGGATAGAAATATGCTATCGTTTTTGTCTTGTGACATCTAGT	1440
DB	1381	TGCAAAATCTGTATGGATAGAAATATGCTATCGTTTTTGTCTTGTGACATCTAGT	1440
QY	1441	ACTTGTAAACAATGTGCTGAAGCAGTTGACAAAGTGTCCCATGTGTACACAGCT	1500
DB	1441	ACTTGTAAACAATGTGCTGAAGCAGTTGACAAAGTGTCCCATGTGTACACAGCT	1500
QY	1501	TTCAAGCAAAAAATTTTATGTTCTTAATCTAATCTATAGTAGGCGATGTTTGTCT	1560
DB	1501	TTCAAGCAAAAAATTTTATGTTCTTAATCTAATCTATAGTAGGCGATGTTTGTCT	1560
QY	1561	TATTACCTTGATGATGCTGATGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA	1620
DB	1561	TATTACCTTGATGATGCTGATGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA	1620
QY	1621	TAGCAATTTCTACCAGTAGGAAAAAATGTACATGGCAGTGTCTTAGTTGGCAATA	1680
DB	1621	TAGCAATTTCTACCAGTAGGAAAAAATGTACATGGCAGTGTCTTAGTTGGCAATA	1680
QY	1681	ATCTTTGAATTTCTGATTTTTCAGGGTATTAGCTGATTTATCCATTTTCTTACT	1740
DB	1681	ATCTTTGAATTTCTGATTTTTCAGGGTATTAGCTGATTTATCCATTTTCTTACT	1740



```
QY 1501 TTCAGCAAAATTTTATGCTCTTAATCTAACTATAGTAGGCATGTTATGTTGTTCT 1560
|||||
Db 1501 TTCAGCAAAATTTTATGCTCTTAATCTAACTATAGTAGGCATGTTATGTTGTTCT 1560
QY 1561 TATPACCCGTGATGAATGTGATGTGACGACGCTTTAAGTAATCAGGATGAATCCAT 1620
|||||
Db 1561 TATPACCCGTGATGAATGTGATGTGACGACGCTTTAAGTAATCAGGATGAATCCAT 1620
QY 1621 TAGCATTTGCTACCAAGTAGGAAAAAATGTACATGCGAGTGTGTTAGTTGGCAATATA 1680
|||||
Db 1621 TAGCATTTGCTACCAAGTAGGAAAAAATGTACATGCGAGTGTGTTAGTTGGCAATATA 1680
QY 1681 ATCTTTGAATTTCTTGATTTTTCAGGGTATTAGCTGTATTATPCCATTTTTTTTACTGTTA 1740
|||||
Db 1681 ATCTTTGAATTTCTTGATTTTTCAGGGTATTAGCTGTATTATPCCATTTTTTTTACTGTTA 1740
QY 1741 TTTAATTTGAACCATAGACTAAGATAAGAACATCATACTATATACTGAACAAATGTT 1800
|||||
Db 1741 TTTAATTTGAACCATAGACTAAGATAAGAACATCATACTATATACTGAACAAATGTT 1800
QY 1801 ATTCTAGTATATCATTTAATTTCTAAGTGTAACTGAATTAATCATCTGGATTTTTTAT 1860
|||||
Db 1801 ATTCTAGTATATCATTTAATTTCTAAGTGTAACTGAATTAATCATCTGGATTTTTTAT 1860
QY 1861 TCTTTTCAGATAGGCTTAAACCAATGGAGCTTTCTGTATATATAAATGTGGAGATTAGAGTTA 1920
|||||
Db 1861 TCTTTTCAGATAGGCTTAAACCAATGGAGCTTTCTGTATATATAAATGTGGAGATTAGAGTTA 1920
QY 1921 ATCTCCCAATCACATAATTTGTTGTGTGAAAAAGGAATAAATGTTCCATGCTGGTG 1980
|||||
Db 1921 ATCTCCCAATCACATAATTTGTTGTGTGAAAAAGGAATAAATGTTCCATGCTGGTG 1980
QY 1981 GAAAGATAGAGATTTTCTTAGAGCTTGGTGTGTTGTTTGGATTTCTGTCATTTTCT 2040
|||||
Db 1981 GAAAGATAGAGATTTTCTTAGAGCTTGGTGTGTTGTTTGGATTTCTGTCATTTTCT 2040
QY 2041 T 2041
Db 2041 T 2041
```

```
RESULT 15
US-09-201-932-3
; Sequence 3, Application US/09201932
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003004
; CURRENT APPLICATION NUMBER: US/09/201,932
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2540)...(2540)
; OTHER INFORMATION: N may be any nucleotide
```

US-09-201-932-3

```
Query Match 38.0%; Score 1990; DB 16; Length 2540;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAAAGTGGCAAGTCCCTATTTTCAAGAGAAGATGACTTTTAAACAGTTTTGAAGATCT 60
Db 1 GAAAAGTGGCAAGTCCCTATTTTCAAGAGAAGATGACTTTTAAACAGTTTTGAAGATCT 60
QY 61 AAAAATCTGTGACCTGCAGACATCAATAGGAGAGAGATTTGTAGAGAGTTTATAGA 120
Db 61 AAAAATCTGTGACCTGCAGACATCAATAGGAGAGAGATTTGTAGAGAGTTTATAGA 120
QY 121 TTAATAAATCTTTGCTAAATTTTCCAAAGTGTAGTCTCTGTTTCAAGCATCAACACTGGCACA 180
Db 121 TTAATAAATCTTTGCTAAATTTTCCAAAGTGTAGTCTCTGTTTCAAGCATCAACACTGGCACA 180
QY 181 GCAGGTTTCTTTTATCTAGTGGTGAAGAGATACCGTGGGTGCTTTAGTTGTCTATGAGCT 240
Db 181 GCAGGTTTCTTTTATCTAGTGGTGAAGAGATACCGTGGGTGCTTTAGTTGTCTATGAGCT 240
QY 241 GTAGATAGATGCCATATGGAGACTCAGCAGTTGGAAGACACAGGAAAGTATCCCAAT 300
Db 241 GTAGATAGATGCCATATGGAGACTCAGCAGTTGGAAGACACAGGAAAGTATCCCAAT 300
QY 301 TGCAGATTTATCAACGGCTTTTATCTTGAATAATAGTGCCACGACGCTACAAATTTCTGT 360
Db 301 TGCAGATTTATCAACGGCTTTTATCTTGAATAATAGTGCCACGACGCTACAAATTTCTGT 360
QY 361 ATCCAGAATGTCAGTACAAAGTTGAAAATCTATCTGGGAAGCAGAGATCATTTTGCCTTA 420
Db 361 ATCCAGAATGTCAGTACAAAGTTGAAAATCTATCTGGGAAGCAGAGATCATTTTGCCTTA 420
QY 421 GACAGCCATCTGAGACACATCCAGACTATCTTTTGAGAACTCTGGAAGCTGAGATATA 480
Db 421 GACAGCCATCTGAGACACATCCAGACTATCTTTTGAGAACTCTGGAAGCTGAGATATA 480
QY 481 TCAGACACCATATACCCGAGGAACCTGCTCATGTATAGTGAAGAGCTAGATATAAGTCC 540
Db 481 TCAGACACCATATACCCGAGGAACCTGCTCATGTATAGTGAAGAGCTAGATATAAGTCC 540
QY 541 TTTTCAAGACTGCCAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTCTGGACTC 600
Db 541 TTTTCAAGACTGCCAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTCTGGACTC 600
QY 601 TACTACACAGGTATTGGTGACCAAGTGCAGTCTTTTGTGTTGGTGGAAAACTGAAAAAT 660
Db 601 TACTACACAGGTATTGGTGACCAAGTGCAGTCTTTTGTGTTGGTGGAAAACTGAAAAAT 660
QY 661 TGGGAACCTTGTGATCGTCCCTGGTGCAGAACACAGGCGACACTTTCTTAATTTCTTTT 720
Db 661 TGGGAACCTTGTGATCGTCCCTGGTGCAGAACACAGGCGACACTTTCTTAATTTCTTTT 720
QY 721 GTTTTGGGCGGAATCTTAAATATTCGAAGTGAATCTGTAGTCTGTGAGTTCTTGATAGAA 780
Db 721 GTTTTGGGCGGAATCTTAAATATTCGAAGTGAATCTGTAGTCTGTGATAGAA 780
QY 781 TTTCCAAATTCACAAATCTTCCAAAGAAATCCATCCATGGCAGATATTAAGACACGGATC 840
Db 781 TTTCCAAATTCACAAATCTTCCAAAGAAATCCATCCATGGCAGATATTAAGACACGGATC 840
QY 841 TTTACTTTTGGGACATGGATATACTACGTTAACAGGACGACCTTGCAGAGCTGGATTT 900
Db 841 TTTACTTTTGGGACATGGATATACTACGTTAACAGGACGACCTTGCAGAGCTGGATTT 900
QY 901 TATGCTTTAGTGAAGGTGATATAAAGTCTTCTTCTGTTGGAGGAGGCTTAAGTAT 960
Db 901 TATGCTTTAGTGAAGGTGATATAAAGTCTTCTTCTGTTGGAGGAGGCTTAAGTAT 960
QY 961 TGGAAAGCCAGTGAAGACCCCTTGGGAACAAATGCTAAATGGTATCCAGGGTCAAAATAT 1020
Db 961 TGGAAAGCCAGTGAAGACCCCTTGGGAACAAATGCTAAATGGTATCCAGGGTCAAAATAT 1020
```



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 9, 2002, 20:05:26 ; Search time 87 Seconds  
(without alignments)  
9446.005 Million cell updates/sec

Title: US-09-974-592-3  
Perfect score: 5232  
Sequence: 1 gaaaagtggaagtcctca.....tcaaaaaaaaaaaaaaag 5232

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 205966 seqs, 78536166 residues

Word size : 0

Total number of hits satisfying chosen parameters: 411932

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending\_Patents\_NA\_New.\*  
1: /cgn2\_6/ptodata/1/pna/PCT\_NEW\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq.\*  
7: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	314	6.0	315	US-09-513-999C-29306	Sequence 29306, A
2	151	2.9	190	US-09-513-999C-28292	Sequence 28292, A
3	85	1.6	237	US-09-513-999C-25994	Sequence 25994, A
4	79	1.5	237	US-09-513-999C-26027	Sequence 26027, A
5	79	1.5	276820	US-10-271-416-9	Sequence 9, Appli
6	77	1.5	271	US-09-513-999C-20475	Sequence 20475, A
7	76	1.5	100267	US-10-240-425-1470	Sequence 1470, Ap
8	70	1.3	5574	US-09-513-999C-18190	Sequence 396, App
9	69	1.3	212	US-09-513-999C-32057	Sequence 32057, A
10	69	1.3	231	US-09-513-999C-1101	Sequence 1101, Ap
11	69	1.3	133760	US-10-271-416-1	Sequence 1, Appli
12	69	1.3	304905	US-10-240-425-1102	Sequence 1102, Ap
13	67	1.3	134292	US-09-539-333D-1	GENERAL INFORMATI
14	67	1.3	319608	US-09-539-333D-1	Sequence 1, Appli
15	67	1.3	319608	US-09-539-333D-1	Sequence 27025, A
16	66	1.3	170	US-09-513-999C-27025	Sequence 27025, A
17	66	1.3	191	US-09-513-999C-22797	Sequence 22797, A
18	66	1.3	192	US-09-513-999C-22123	Sequence 22123, A
19	66	1.3	289	US-09-513-999C-19193	Sequence 19193, A
20	66	1.3	26928	US-10-240-851-6	Sequence 6, Appli
21	65	1.2	33769	US-10-240-851-8	Sequence 8, Appli
22	63	1.2	137	US-09-513-999C-27657	Sequence 27657, A
23	63	1.2	278	US-09-513-999C-32453	Sequence 32453, A
24	61	1.2	215	US-09-513-999C-22153	Sequence 22153, A
25	61	1.2	445	US-09-513-999C-23555	Sequence 23555, A
26	60	1.1	1697	US-10-240-425-1450	Sequence 1450, Ap

27	60	1.1	8705	6	US-10-240-851-10	Sequence 10, Appli
28	59	1.1	276820	6	US-10-271-416-9	Sequence 9, Appli
c 29	59	1.1	97	5	US-09-513-999C-20263	Sequence 20263, A
c 30	59	1.1	97	5	US-09-513-999C-20264	Sequence 20264, A
c 31	59	1.1	147	5	US-09-513-999C-20249	Sequence 20249, A
c 32	59	1.1	148	5	US-09-513-999C-20098	Sequence 20098, A
c 33	59	1.1	33769	6	US-10-240-851-8	Sequence 8, Appli
c 34	59	1.1	201143	6	US-10-240-425-1099	Sequence 1099, Ap
c 35	57	1.1	196	5	US-09-513-999C-34689	Sequence 34689, A
c 36	56	1.1	152	5	US-09-513-999C-27160	Sequence 27160, A
c 37	55	1.1	133	5	US-09-513-999C-17546	Sequence 17546, A
c 38	55	1.1	199	5	US-09-513-999C-19906	Sequence 19906, A
c 39	54	1.0	239	5	US-09-513-999C-24738	Sequence 24738, A
c 40	54	1.0	311	5	US-09-513-999C-14837	Sequence 14837, A
c 41	54	1.0	16553	6	US-10-264-237-2851	Sequence 2851, Ap
c 42	54	1.0	201143	6	US-10-240-425-1099	Sequence 1099, Ap
c 43	53	1.0	149	5	US-09-513-999C-32581	Sequence 32581, A
c 44	53	1.0	167	5	US-09-513-999C-20746	Sequence 20746, A
c 45	53	1.0	202	5	US-09-513-999C-17350	Sequence 17350, A

ALIGNMENTS

RESULT 1  
US-09-513-999C-29306  
; Sequence 29306, Application US/09513999C  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: 59 US2 REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 29306  
; LENGTH: 315  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-513-999C-29306

Query Match	6.0%;	Score 314;	DB 5;	Length 315;
Best Local Similarity	100.0%;	Pred. No. 6.3e-102;	Mismatches 0;	Indels 0;
Matches 314;	Conservative 0;			
QY 4005	CATTAAATTCCTCTAAAACTTGATGTTAGAGTTAAGCAAGACTTTTCTTCTCTCT	4064		
Db 1	CATTAAATTCCTCTAAAACTTGATGTTAGAGTTAAGCAAGACTTTTCTTCTCTCT	60		
QY 4065	CCATGAGTTGTGAATTTAATGCACACGCTGATGGGTAAACAAGTTATTTTAAAGAT	4124		
Db 61	CCATGAGTTGTGAATTTAATGCACACGCTGATGGGTAAACAAGTTATTTTAAAGAT	120		
QY 4125	TGTTTGAAGTCTGTGCTTCAGGTTCTTAAATCAGTCCAGCTCCCACTTCTAATCA	4184		
Db 121	TGTTTGAAGTCTGTGCTTCAGGTTCTTAAATCAGTCCCACTTCTAATCA	180		
QY 4185	AAATTTTGAGACTTAAACAGCACTTCTGCTGTGTTTGAACATATAAAAGACCCGGATCTTT	4244		
Db 181	AAATTTTGAGACTTAAACAGCACTTCTGCTGTGTTTGAACATATAAAAGACCCGGATCTTT	240		
QY 4245	TCCATCTAATTCGCAAAAATTGATCATTTGCAAAAGTCAAACTATAGCATATCAAAAT	4304		
Db 241	TCCATCTAATTCGCAAAAATTGATCATTTGCAAAAGTCAAACTATAGCATATCAAAAT	300		
QY 4305	CTTTTCCCTCCCTCC 4318			
Db 301	CTTTTCCCTCCCTCC 314			



```
RESULT 2
US-09-513-999C-28292
; Sequence 28292, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 28292
; LENGTH: 190
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 173
; OTHER INFORMATION: b-c or g or t
US-09-513-999C-28292

Query Match          2.9%; Score 151; DB 5; Length 190;
Best Local Similarity 100.0%; Pred. No. 1.2e-44;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2121 ATACTATCGAGCCAAACATGCTACTGACATGGAAGATGTCAAAGATATGTTAAAGTGTAAAA 2180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 ATACTATCGAGCCAAACATGCTACTGACATGGAAGATGTCAAAGATATGTTAAAGTGTAAAA 60

QY 2181 TGCAGGTGCGAAACACTATGATCTAGTCTGAGCCAGATCAAAGTATGTTGTTTAAATA 2240
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 TGCAGGTGCGAAACACTATGATCTAGTCTGAGCCAGATCAAAGTATGTTGTTTAAATA 120

QY 2241 TGCATAGACAAAGATTTGGAAAGATATAC 2271
      |||||||||||||||||||||||||||||||||||||||||||
Db 121 TGCATAGACAAAGATTTGGAAAGATATAC 151

RESULT 3
US-09-513-999C-25994/c
; Sequence 25994, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 25994
; LENGTH: 237
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-25994

Query Match          1.6%; Score 85; DB 5; Length 237;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4947 TGGCTCACGCTGTAATCCAGCAGCTTTGGAGGCTGAGGAGGTGGATCAGGAGTCTCAG 5006
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 124 TGGCTCACGCTGTAATCCAGCAGCTTTGGAGGCTGAGGAGGTGGATCAGGAGTCTCAG 65

QY 5007 GAGATCGAGACCATCTGGCTAACA 5031
      |||||||||||||||||||||||||||||||||||||||
Db 5007 GAGATCGAGACCATCTGGCTAACA 5031
```

```
Db 64 GAGATCGAGACCATCTGGCTAACA 40
      |||||||||||||||||||||||||||||||||||

RESULT 4
US-09-513-999C-26027/c
; Sequence 26027, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 26027
; LENGTH: 237
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 119
; OTHER INFORMATION: r-a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 139
; OTHER INFORMATION: r-a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 146
; OTHER INFORMATION: m-a or c
US-09-513-999C-26027

Query Match          1.5%; Score 79; DB 5; Length 237;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4953 ACGCCTGTAATCCAGCAGCTTTGGAGGCTGAGGAGGTGGATCAGGAGTCTCAGGAGATC 5012
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 118 ACGCCTGTAATCCAGCAGCTTTGGAGGCTGAGGAGGTGGATCAGGAGTCTCAGGAGATC 59

QY 5013 GAGACCATCTGGCTAACA 5031
      |||||||||||||||||||
Db 58 GAGACCATCTGGCTAACA 40

RESULT 5
US-10-271-416-9/c
; Sequence 9, Application US/10271416
; GENERAL INFORMATION:
; APPLICANT: Keith, Tim
; APPLICANT: Little, Randall D.
; APPLICANT: Van Eerdewegh, Paul
; APPLICANT: Dupuis, Josee
; APPLICANT: Del Maestro, Richard G.
; APPLICANT: Allen, Kristina
; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO RESPIRATORY DISEASES AND OBESITY
; FILE REFERENCE: 2976-4045
; CURRENT APPLICATION NUMBER: US/10/271,416
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/328,424
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 276820
; TYPE: DNA
; ORGANISM: Homo sapien
```

```
; FEATURE:
; NAME/KEY: conflict
; LOCATION: (167043)...(167043)
; OTHER INFORMATION: Y-C or T
US-10-271-416-9

Query Match          1.5%; Score 79; DB 6; Length 276820;
Best Local Similarity 100.0%; Pred. No. 4e-20;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5084 GGGCGCCTGTAGTCCACACTACTCGGGAGGCTGAGGCGAGGAGATGGTGTGAACCCGGGA 5143
Db 276166 GGGCGCCTGTAGTCCACACTACTCGGGAGGCTGAGGCGAGGAGATGGTGTGAACCCGGGA 276107

QY 5144 GCGAGAGCTTCAGTGAGC 5162
Db 276106 GCGAGAGCTTCAGTGAGC 276088

RESULT 6
US-09-513-999C-20475/c
; Sequence 20475, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513.999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 20475
; LENGTH: 271
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 261
; OTHER INFORMATION: s-g or c
US-09-513-999C-20475

Query Match          1.5%; Score 77; DB 5; Length 271;
Best Local Similarity 100.0%; Pred. No. 1.1e-18;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5062 AAAATTAGCGGGCGTGTGGCGGCGCTGTAGTCCAGCTACTCGGGAGGCTGAGGCA 5121
Db 148 AAAATTAGCGGGCGTGTGGCGGCGCTGTAGTCCAGCTACTCGGGAGGCTGAGGCA 89

QY 5122 GGAGAAATGGTGTGAACC 5138
Db 88 GGAGAAATGGTGTGAACC 72

RESULT 7
US-10-240-425-1470/c
; Sequence 1470, Application US/10240425
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240.425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 17963
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1470
; LENGTH: 100267
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. U89337
US-10-240-425-1470

Query Match          1.5%; Score 76; DB 6; Length 100267;
Best Local Similarity 100.0%; Pred. No. 5.8e-19;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4983 GAGCGAGTGGATCACGAGGTGAGGATCGAGATCGAGACCATCCTGGCTAACACGGTGAACCC 5042
Db 18022 GAGCGAGTGGATCACGAGGTGAGGATCGAGATCGAGACCATCCTGGCTAACACGGTGAACCC 17963

QY 5043 CGTCTCTACTAAAAA 5058
Db 17962 CGTCTCTACTAAAAA 17947

RESULT 8
US-10-240-425-396/c
; Sequence 396, Application US/10240425
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240.425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 396
; LENGTH: 5574
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. AF055481
US-10-240-425-396

Query Match          1.3%; Score 70; DB 6; Length 5574;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5077 TGGTGGCGGGCGCTGTAGTCCAGCTACTCGGAGGCTGAGGAGGAGATGGTGTGAA 5136
Db 1178 TGGTGGCGGGCGCTGTAGTCCAGCTACTCGGAGGCTGAGGAGGAGATGGTGTGAA 1119

QY 5137 CCCGGGAGGC 5146
Db 1118 CCCGGGAGGC 1109

RESULT 9
US-09-513-999C-18190
; Sequence 18190, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
```

```
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1470
; LENGTH: 100267
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. U89337
US-10-240-425-1470

Query Match          1.5%; Score 76; DB 6; Length 100267;
Best Local Similarity 100.0%; Pred. No. 5.8e-19;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4983 GAGCGAGTGGATCACGAGGTGAGGATCGAGATCGAGACCATCCTGGCTAACACGGTGAACCC 5042
Db 18022 GAGCGAGTGGATCACGAGGTGAGGATCGAGATCGAGACCATCCTGGCTAACACGGTGAACCC 17963

QY 5043 CGTCTCTACTAAAAA 5058
Db 17962 CGTCTCTACTAAAAA 17947

RESULT 8
US-10-240-425-396/c
; Sequence 396, Application US/10240425
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240.425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 396
; LENGTH: 5574
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. AF055481
US-10-240-425-396

Query Match          1.3%; Score 70; DB 6; Length 5574;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5077 TGGTGGCGGGCGCTGTAGTCCAGCTACTCGGAGGCTGAGGAGGAGATGGTGTGAA 5136
Db 1178 TGGTGGCGGGCGCTGTAGTCCAGCTACTCGGAGGCTGAGGAGGAGATGGTGTGAA 1119

QY 5137 CCCGGGAGGC 5146
Db 1118 CCCGGGAGGC 1109

RESULT 9
US-09-513-999C-18190
; Sequence 18190, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
```

```
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 18190
; LENGTH: 212
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 132
; OTHER INFORMATION: m-a or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 184
; OTHER INFORMATION: w-a or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 200
; OTHER INFORMATION: w-a or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 202
; OTHER INFORMATION: k-g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 203
; OTHER INFORMATION: y-c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 212
; OTHER INFORMATION: r-a or g
US-09-513-999C-18190

Query Match
Best Local Similarity 100.0%; Score 69; DB 5; Length 212;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5062 AAAATTAGCGGCGGTGGTGGCGGCGCTGTAGTCCCGAGCTACTCCGAGGCTGAGGCA 5121
|||||
Db 18 AAAATTAGCGGCGGTGGTGGCGGCGCTGTAGTCCCGAGCTACTCCGAGGCTGAGGCA 77

QY 5122 GGAGAAATGG 5130
|||||
Db 78 GGAGAAATGG 86

RESULT 10
US-09-513-999C-32057
; Sequence 32057, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 32057
; LENGTH: 231
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
```

```
; NAME/KEY: misc_feature
; LOCATION: 215
; OTHER INFORMATION: s-g or c
US-09-513-999C-32057

Query Match
Best Local Similarity 100.0%; Score 69; DB 5; Length 231;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4989 GGTGGATCAGGAGGTGAGGATCGAGACCATCTGGCTAACACGGTGAACCCCGTCTC 5048
|||||
Db 22 GGTGGATCAGGAGGTGAGGATCGAGACCATCTGGCTAACACGGTGAACCCCGTCTC 81

QY 5049 TACTAAAAA 5057
|||||
Db 82 TACTAAAAA 90

RESULT 11
US-10-240-425-1101
; Sequence 1101, Application US/10240425
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Bolland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240,425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1101
; LENGTH: 133760
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. AL031737
US-10-240-425-1101

Query Match
Best Local Similarity 100.0%; Score 69; DB 6; Length 133760;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5062 AAAATTAGCGGCGGTGGTGGCGGCGCTGTAGTCCCGAGCTACTCCGAGGCTGAGGCA 5121
|||||
Db 120084 AAAATTAGCGGCGGTGGTGGCGGCGCTGTAGTCCCGAGCTACTCCGAGGCTGAGGCA 120143

QY 5122 GGAGAAATGG 5130
|||||
Db 120144 GGAGAAATGG 120152

RESULT 12
US-10-271-416-1
; Sequence 1, Application US/10271416
; GENERAL INFORMATION:
; APPLICANT: Keith, Tim
; APPLICANT: Little, Randall D.
; APPLICANT: Van Eerdewegh, Paul
; APPLICANT: Dupuis, Josee
; APPLICANT: Del Mastro, Richard G.
; APPLICANT: Allen, Kristina
; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO RESPIRATORY DISEASES AND OBESITY
; FILE REFERENCE: 2976-4045
```

; CURRENT APPLICATION NUMBER: US/10/271.416  
; CURRENT FILING DATE: 2002-10-11  
; PRIOR APPLICATION NUMBER: 60/328,424  
; PRIOR FILING DATE: 2001-10-11  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 304905  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-271-416-1

Query Match 1.3%; Score 69; DB 6; Length 304905;  
Best Local Similarity 100.0%; Pred. No. 1.3e-16;  
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5062 AAAATTAGCGGCGTGTGGGGCGCTGTAGTCCAGCTACTCGGAGGCTGAGGCA 5121  
|||||  
Db 25099 AAAATTAGCGGCGTGTGGGGCGCTGTAGTCCAGCTACTCGGAGGCTGAGGCA 25158  
|||||  
QY 5122 GGAGAAATGG 5130  
|||||  
Db 25159 GGAGAAATGG 25167  
|||||

RESULT 13  
US-10-240-425-1102  
; Sequence 1102, Application US/10240425  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Amanda  
; APPLICANT: Boland, Joseph F.  
; APPLICANT: Lord, Reginald V.  
; APPLICANT: Alvarez, Chris  
; APPLICANT: Wetzel, Jon C.  
; APPLICANT: Scherf, Uwe  
; APPLICANT: Vockley, Joseph G.  
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue  
; FILE REFERENCE: 44921-5026  
; CURRENT APPLICATION NUMBER: US/10/240.425  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: PCT/US01/09847  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: US 60/193,446  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 1588  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1102  
; LENGTH: 134292  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. AL031983  
US-10-240-425-1102

Query Match 1.3%; Score 67; DB 6; Length 134292;  
Best Local Similarity 100.0%; Pred. No. 7.8e-16;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4952 GGATCAGGTCAGGAGTCGAGACCATCTGGCTACACAGGTGAACCCCGTCTCTAC 5051  
|||||  
Db 113318 GGATCAGGTCAGGAGTCGAGACCATCTGGCTACACAGGTGAACCCCGTCTCTAC 113377  
|||||  
QY 5052 TAAAAAA 5058  
|||||  
Db 113378 TAAAAAA 113384  
|||||

RESULT 14  
US-09-539-333D-1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilya

; APPLICANT: Bougueleret, Lydie  
; APPLICANT: Bihain, Bernard  
; APPLICANT: Essioux, Laurent  
; TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS  
; FILE REFERENCE: GENSET.047AUS  
; CURRENT APPLICATION NUMBER: US/09/539.333D  
; CURRENT FILING DATE: 2000-03-30  
; PRIOR APPLICATION NUMBER: US 60/126,903  
; PRIOR FILING DATE: 1999-03-30  
; PRIOR APPLICATION NUMBER: US 60/131,971  
; PRIOR FILING DATE: 1999-04-30  
; PRIOR APPLICATION NUMBER: US 60/132,065  
; PRIOR FILING DATE: 1999-04-30  
; PRIOR APPLICATION NUMBER: US 60/143,928  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: US 60/145,915  
; PRIOR FILING DATE: 1999-07-27  
; PRIOR APPLICATION NUMBER: US 60/146,453  
; PRIOR FILING DATE: 1999-07-29  
; PRIOR APPLICATION NUMBER: US 60/146,452  
; PRIOR FILING DATE: 1999-07-29  
; PRIOR APPLICATION NUMBER: US 60/162,288  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: US 09/416,384  
; PRIOR FILING DATE: 1999-10-12  
; NUMBER OF SEQ ID NOS: 231  
; SOFTWARE: Patent.pm  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 110222  
; OTHER INFORMATION: polymorphic base G or T  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 111978  
; OTHER INFORMATION: polymorphic base A or G  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 112468  
; OTHER INFORMATION: polymorphic base G or T  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 117324..117327  
; OTHER INFORMATION: deletion ACTT  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 118972  
; OTHER INFORMATION: polymorphic base C or T  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 119160..119161  
; OTHER INFORMATION: deletion TT  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 119316  
; OTHER INFORMATION: polymorphic base C or T  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 119321  
; OTHER INFORMATION: polymorphic base A or G  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 119526  
; OTHER INFORMATION: polymorphic base A or G  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 120573  
; OTHER INFORMATION: polymorphic base A or G  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 121527  
; OTHER INFORMATION: polymorphic base A or C  
; FEATURE:  
; NAME/KEY: allele

LOCATION: 126105  
OTHER INFORMATION: polymorphic base C or T  
FEATURE:  
NAME/KEY: allele  
LOCATION: 129789  
OTHER INFORMATION: polymorphic base C or G  
FEATURE:  
NAME/KEY: allele  
LOCATION: 130777  
OTHER INFORMATION: polymorphic base A or G  
FEATURE:  
NAME/KEY: allele  
LOCATION: 136942..136944  
OTHER INFORMATION: deletion ATT  
FEATURE:  
NAME/KEY: allele  
LOCATION: 143839  
OTHER INFORMATION: polymorphic base A or T  
FEATURE:  
NAME/KEY: allele  
LOCATION: 146668  
OTHER INFORMATION: polymorphic base C or T  
FEATURE:  
NAME/KEY: allele  
LOCATION: 147281  
OTHER INFORMATION: polymorphic base C or T  
FEATURE:  
NAME/KEY: allele  
LOCATION: 147505  
OTHER INFORMATION: polymorphic base G or T  
FEATURE:  
NAME/KEY: allele  
LOCATION: 148183  
OTHER INFORMATION: deletion T  
FEATURE:  
NAME/KEY: allele  
LOCATION: 148372  
OTHER INFORMATION: polymorphic base A or C  
FEATURE:  
NAME/KEY: allele  
LOCATION: 149012  
OTHER INFORMATION: polymorphic base A or G  
FEATURE:  
NAME/KEY: allele  
LOCATION: 149113  
OTHER INFORMATION: polymorphic base C or T  
FEATURE:  
NAME/KEY: allele  
LOCATION: 151637  
OTHER INFORMATION: polymorphic base A or G  
FEATURE:  
NAME/KEY: allele  
LOCATION: 151748  
OTHER INFORMATION: deletion G  
FEATURE:  
NAME/KEY: allele  
LOCATION: 151769  
OTHER INFORMATION: polymorphic base A or G  
FEATURE:  
NAME/KEY: allele  
LOCATION: 151847  
OTHER INFORMATION: polymorphic base C or T  
FEATURE:  
NAME/KEY: allele  
LOCATION: 152691  
OTHER INFORMATION: polymorphic base A or C  
FEATURE:  
NAME/KEY: allele  
LOCATION: 152766  
OTHER INFORMATION: polymorphic base A or G  
FEATURE:  
NAME/KEY: allele  
LOCATION: 153046

OTHER INFORMATION: polymorphic base C or T  
FEATURE:  
NAME/KEY: allele  
LOCATION: 153123  
OTHER INFORMATION: polymorphic base A or G  
FEATURE:  
NAME/KEY: allele  
LOCATION: 153925  
OTHER INFORMATION: polymorphic base C or T  
FEATURE:  
NAME/KEY: allele  
LOCATION: 153977  
OTHER INFORMATION: polymorphic base G or T  
FEATURE:  
NAME/KEY: allele  
LOCATION: 154502  
OTHER INFORMATION: polymorphic base C or T  
FEATURE:  
NAME/KEY: allele  
LOCATION: 154677  
OTHER INFORMATION: polymorphic base A or G  
FEATURE:  
NAME/KEY: allele  
LOCATION: 154879  
OTHER INFORMATION: polymorphic base C or T  
FEATURE:  
NAME/KEY: allele  
LOCATION: 154918  
OTHER INFORMATION: polymorphic base G or T  
FEATURE:  
NAME/KEY: allele  
LOCATION: 155802  
OTHER INFORMATION: polymorphic base C or T  
FEATURE:  
NAME/KEY: allele  
LOCATION: 156448  
OTHER INFORMATION: polymorphic base A or G  
FEATURE:  
NAME/KEY: allele  
LOCATION: 157238  
OTHER INFORMATION: polymorphic base A or C  
FEATURE:  
NAME/KEY: allele  
LOCATION: 157897  
OTHER INFORMATION: polymorphic base A or G  
FEATURE:  
NAME/KEY: allele  
LOCATION: 158172  
OTHER INFORMATION: polymorphic base A or G  
FEATURE:

Query Match 1.3%; Score 67; DB 5; Length 319608;  
Best Local Similarity 100.0%; Pred. No. 6.4e-16;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5062 AAATAGCGGGCGGTGGCGGCGCCTGTAGTCCAGCTACTCGGAGGCTGAGGCA 5121  
|||||  
DB 276617 AAATAGCGGGCGGTGGCGGCGCCTGTAGTCCAGCTACTCGGAGGCTGAGGCA 276676  
|||||

QY 5122 GGAGAT 5128  
|||||  
DB 276677 GGAGAT 276683

RESULT 15  
US-09-539-333D-1  
; Sequence 1, Application US/09539333D  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilya  
; APPLICANT: Bougueret, Lydie  
; APPLICANT: Bihain, Bernard

```

; APPLICANT: Essloux, Laurent
; TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
; FILE REFERENCE: GENSET.047AUS
; CURRENT APPLICATION NUMBER: US/09/539,333D
; CURRENT FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US 60/126,903
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/131,971
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/132,065
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/143,928
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: US 60/145,915
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: US 60/146,453
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/146,452
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/162,288
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/416,384
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 319608
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 31..1107
; OTHER INFORMATION: 5'regulatory region g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1108..1289
; OTHER INFORMATION: exon A g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 14877..14920
; OTHER INFORMATION: exon B g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 18778..18862
; OTHER INFORMATION: exon Bbis g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 25593..25740
; OTHER INFORMATION: exon C g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 29388..29502
; OTHER INFORMATION: exon D g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 29967..30282
; OTHER INFORMATION: exon E g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 64666..64812
; OTHER INFORMATION: exon F g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 65505..65853
; OTHER INFORMATION: exon G g35018 gene
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 65854..67854
; OTHER INFORMATION: 3'regulatory region g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 94124..94964
; OTHER INFORMATION: exon g35017
;
; FEATURE:
; NAME/KEY: exon
; LOCATION: 201188..201234
; OTHER INFORMATION: exon S g35030 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 214676..214793
; OTHER INFORMATION: exon T g35030 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 215702..215746
; OTHER INFORMATION: exon U g35030 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 216836..216915
; OTHER INFORMATION: exon V g35030 gene
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 213818..215818
; OTHER INFORMATION: 3'regulatory region g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 215819..215941
; OTHER INFORMATION: exon R complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 215819..215975
; OTHER INFORMATION: exon Rbis complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 216661..216952
; OTHER INFORMATION: exon Qbis complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 216661..217061
; OTHER INFORMATION: exon Q complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 217027..217061
; OTHER INFORMATION: exon Q1 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 229647..229742
; OTHER INFORMATION: exon X complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 230408..230721
; OTHER INFORMATION: exon P complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 231272..231412
; OTHER INFORMATION: exon Obis complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 231787..231880
; OTHER INFORMATION: exon O2 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 231870..231879
; OTHER INFORMATION: exon O1 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 234174..234321
; OTHER INFORMATION: exon O complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 237406..237428
; OTHER INFORMATION: exon Nbis complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 239719..239807
; OTHER INFORMATION: exon N2 complement g34872 gene
; FEATURE:
```

```

; NAME/KEY: exon
; LOCATION: 239719..239853
; OTHER INFORMATION: exon N complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 240528..240569
; OTHER INFORMATION: exon M1117 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 240528..240596
; OTHER INFORMATION: exon M1090 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 240528..240617
; OTHER INFORMATION: exon M1069 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 240528..240644
; OTHER INFORMATION: exon M52 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 240528..240824
; OTHER INFORMATION: exon M862 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 240528..240994
; OTHER INFORMATION: exon M692 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 240528..241685
; OTHER INFORMATION: exon M1 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 240800..240993
; OTHER INFORMATION: exon M51 complement g34872 gene
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 241686..243685
; OTHER INFORMATION: 5'regulatory region g34872 gene
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 290652..292652
; OTHER INFORMATION: 3'regulatory region g34665 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 292653..292841
; OTHER INFORMATION: exon B complement g34665 gene

```

```

Query Match      1.3%; Score 67; DB 5; Length 319608;
Best Local Similarity 100.0%; Pred. No. 6.4e-16;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 5062 AAAATTAGCGGCGGTGGTGGCGGCGCTGTAGTCCAGCTACTCGGAGGCTGAGGCA 5121
|||||
Db 276617 AAAATTAGCGGCGGTGGTGGCGGCGCTGTAGTCCAGCTACTCGGAGGCTGAGGCA 276676
|||||

```

```

QY 5122 GGAGAA 5128
|||||
Db 276677 GGAGAA 276683

```

```

Search completed: November 10, 2002, 05:25:04
Job time : 3430 secs

```



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using -sw model

Run on: November 9, 2002, 19:46:46 ; Search time 6593 Seconds  
(without alignments)  
12852.235 Million cell updates/sec.

Title: US-09-974-592-3  
Perfect score: 5232  
Sequence: 1 gaaaggtgacagctcta.....tcaaaaaaaaaaaaaaag 5232

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_Other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	ID	Description
c 1	641	12.3	757	14	BQ007511	BQ007511 UI-H-ED1-
c 2	571	10.9	822	12	BG502660	BG502660 602549490
c 3	567	10.8	1041	13	BM459898	BM459898 AGENCOURT
c 4	551	10.5	784	9	AI628066	AI628066 ty84b02.x
c 5	469	9.0	529	9	AL713196	AL713196 DKFZp686M
c 6	455	8.7	691	14	BM990097	BM990097 UI-H-D10-

7	450	8.6	537	12	BG616695	BG616695 602614908
c 8	434	8.3	462	12	BF510268	BF510268 UI-H-BI4-
c 9	432	8.3	943	12	BG164322	BG164322 602341372
c 10	422	8.1	472	9	AI277821	AI277821 qm60e01.x
c 11	406	7.8	406	9	AI299965	AI299965 qo24a11.x
c 12	406	7.8	508	10	AW665401	AW665401 h190c08.x
c 13	405	7.7	409	10	BE222433	BE222433 hv90g11.x
c 14	398	7.6	413	9	AI681542	AI681542 tx47e09.x
c 15	389	7.4	707	13	BI823020	BI823020 603039619
c 16	371	7.1	447	9	AI418337	AI418337 tg48a12.x
c 17	368	7.0	648	13	BI094339	BI094339 602860253
c 18	366	7.0	446	12	BF754025	BF754025 CM2-CT500
c 19	357	6.8	681	9	AL138255	AL138255 DKF2p547E
c 20	336	6.4	587	10	AW750285	AW750285 PMO-BT058
c 21	320	6.1	360	10	BE220552	BE220552 ht98a01.x
c 22	303	5.8	693	10	BE380045	BE380045 601159359
c 23	296	5.7	852	14	BQ423165	BQ423165 AGENCOURT
c 24	288	5.5	698	12	BG617067	BG617067 602616141
c 25	245	4.7	461	9	AA115728	AA115728 z186h12.r
c 26	243	4.6	885	12	BE896438	BE896438 601439815
c 27	230	4.4	230	9	AA987840	AA987840 cq93f09.s
c 28	230	4.4	288	14	F08325	F08325 HSCZOG051.n
c 29	228	4.4	386	10	AW673379	AW673379 ba33e09.y
c 30	227	4.3	1177	14	BM805359	BM805359 AGENCOURT
c 31	210	4.0	536	9	AU123207	AU123207 AU123207
c 32	207	4.0	494	14	BQ369513	BQ369513 RC3-GN007
c 33	204	3.9	255	9	AA345330	AA345330 EST51334
c 34	203	3.9	320	10	AW807831	AW807831 MR4-ST009
c 35	176	3.4	465	10	AW675725	AW675725 ba33e09.x
c 36	174	3.3	535	9	AI861853	AI861853 tz91a08.x
c 37	172	3.3	337	14	H64979	H64979 yu66a10.s1
c 38	167	3.2	216	12	BE813985	BE813985 QV3-BN004
c 39	165	3.2	270	12	BE815593	BE815593 PMO-BN016
c 40	163	3.1	308	9	AI873852	AI873852 wnt42e07.x
c 41	162	3.1	716	10	AV706807	AV706807 AV706807
c 42	153	2.9	284	9	AA295472	AA295472 EST100639
c 43	149	2.8	993	14	BQ233403	BQ233403 AGENCOURT
c 44	145	2.8	235	14	241329	241329 HSCZOG052.n
c 45	144	2.8	304	9	AI914443	AI914443 wd49b11.x

#### ALIGNMENTS

RESULT 1  
BQ007511/c  
LOCUS BQ007511 757 bp mRNA linear EST 26-MAR-2002  
DEFINITION UI-H-ED1-ayb-b-04-0-UI.s1 NCI\_CGAP\_ED1 Homo sapiens cDNA clone  
IMAGE:5836323 3', mRNA sequence.  
ACCESSION BQ007511  
VERSION BQ007511.1 GI:19732411  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 757)  
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Dr. Jose Mercuende  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Seq primer: M13 FORWARD  
POLYA-Yes.  
FEATURES  
Location/Qualifiers  
1..757

```
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI_CGAP_ED1"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Left Public Bone; Vector: pT7T3-Pac
(Pharmacia) with a modified polylinker; Site_1: Ecor I;
Site_2: Not I; NCI_CGAP_ED1 is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line C55. The library was constructed according to Bonaldo
, Lennon and Soares, Genome Research, 6:791-806, 1996.
First strand cDNA synthesis was primed with an oligo-dT
primer containing a Not I site. Double stranded cDNA was
ligated to an Ecor I adaptor, digested with Not I, and
cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (drr)18 tail. The
sequence tag for this library is GCTCAAGGCT.
TAG_LIB=UI-H-ED1
TAG_TISSUE=chondrosarcoma
TAG_SEQ=CCTCAAGGCT"
BASE COUNT 257 a 141 c 105 g 254 t
ORIGIN
Query Match 12.3%; Score 641; DB 14; Length 757;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1288 AAGACAGTATGCAAGTAGTCAAGTCAGATTCATTACAGAAAGAGATTAGTACTGAA 1347
DB 713 AAAGACAGTATGCAAGTAGTCAAGTCAGATTCATTACAGAAAGAGATTAGTACTGAA 654
QY 1348 GACAGCTAAGGCGCTGCAAGAGGAGAACGCTTGGCAAAATCTGTATGATAGAAATATT 1407
DB 653 GACAGCTAAGGCGCTGCAAGAGGAGAACGCTTGGCAAAATCTGTATGATAGAAATATT 594
QY 1408 GCTATGCTTTTCTCTGTGGACATCTAGTCACCTTGTAAACAATGTGCTGAAGCAGTT 1467
DB 593 GCTATGCTTTTCTCTGTGGACATCTAGTCACCTTGTAAACAATGTGCTGAAGCAGTT 534
QY 1468 GACAAGTGTCCTGCTACACAGTCATTACTTTCAAGCAAAAATTTTATGCTTAA 1527
DB 533 GACAAGTGTCCTGCTACACAGTCATTACTTTCAAGCAAAAATTTTATGCTTAA 474
QY 1528 TCTAACTCTATAGGTCATGTTATGTTCTTATTACCCGATTCATGTTGATGTC 1587
DB 473 TCTAACTCTATAGGTCATGTTATGTTCTTATTACCCGATTCATGTTGATGTC 414
QY 1588 AACTGACTTTAAGTAATCAGGATTGAATCCATTAGCATTTGTACCAAGTAGCAAAAAA 1647
DB 413 AACTGACTTTAAGTAATCAGGATTGAATCCATTAGCATTTGTACCAAGTAGCAAAAAA 354
QY 1648 AATGTACATGGCAGTGTGTTAGTGGCAATATAATCTTTGAAATTTCTTGATTTTCAGGG 1707
DB 353 AATGTACATGGCAGTGTGTTAGTGGCAATATAATCTTTGAAATTTCTTGATTTTCAGGG 294
QY 1708 TATTAGCTGATTTATCCATTTTACTGTTTATTTAAATGAACCATAGACTAAGAATA 1767
DB 293 TATTAGCTGATTTATCCATTTTACTGTTTATTTAAATGAACCATAGACTAAGAATA 234
QY 1768 AGAAGCATCATATAACTGAACACAATGTGTATTTCATAGTATCTGATTTAATTTCTA 1827
DB 233 AGAAGCATCATATAACTGAACACAATGTGTATTTCATAGTATCTGATTTAATTTCTA 174
QY 1828 AGTGAAGTGAATTAATCATCTGGAATTTTATTTCTTTTCAGATAGGCTTAACAAATGGA 1887
DB 173 AGTGAAGTGAATTAATCATCTGGAATTTTATTTCTTTTCAGATAGGCTTAACAAATGGA 114
QY 1888 GCTTTCTGTATATAATGTGGAGATTAGAGTTAATCTCCC 1928
|||||
```

```
Db 113 GCTTCTGTATATAAATGTGGAGATTAGACTTAATCTCCCC 73
RESULT 2
BG502660
LOCUS DEFINITION 822 bp mRNA linear EST 27-MAR-2001
602549490F1 NTH_MGC_61 Homo sapiens cDNA clone IMAGE:4657102 5',
mRNA sequence.
ACCESSION BG502660
VERSION BG502660
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 822)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1449 row: C column: 23
High quality sequence stop: 670.
FEATURES
Location/Qualifiers
1..822
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4657102"
/tissue_type="embryonal carcinoma"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: Testis; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccattggcc); Site_2: SfiI (ggccattggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGGGCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCGCGCATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."
BASE COUNT 236 a 161 c 201 g 222 t 2 others
ORIGIN
```

```
Query Match 10.9%; Score 571; DB 12; Length 822;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 184 GGTTTCTTTTACTGTTGAAGGAGATACGTCGCGTGTGTTAGTGTCTATGCGAGCTGTA 243
DB 1 GGTTTCTTTTACTGTTGAAGGAGATACGTCGCGTGTGTTAGTGTCTATGCGAGCTGTA 60
QY 244 GATAGTGGCAATATGGAGACTCAGCAGTTGGAAGACACAGAGAAAGTATCCCCAATTGC 303
DB 61 GATAGTGGCAATATGGAGACTCAGCAGTTGGAAGACACAGAGAAAGTATCCCCAATTGC 120
QY 304 AGATTTATCAAGCGCTTTTATCTTGAATAATAGTGGCAGCAGCTCTACAAATCTGTAATC 363
DB 121 AGATTTATCAAGCGCTTTTATCTTGAATAATAGTGGCAGCAGCTCTACAAATCTGTAATC 180
QY 364 CAGAATGGTTCAGTACAAAGTGTAAACTATCTGGGAAGCAGAGATCATTTTGGCTTAGAC 423
DB 181 CAGAATGGTTCAGTACAAAGTGTAAACTATCTGGGAAGCAGAGATCATTTTGGCTTAGAC 240
```

```
QY 424 AGCCATCTGAGACACATGACGACTATCTTTTGAGAACTGGCAGGTTGTAGATATATCA 483
|||||
Db 241 AGCCATCTGAGACACATGACGACTATCTTTTGAGAACTGGCAGGTTGTAGATATCA 300
QY 484 GACACATATACCCGAGGAACTGCGCATGTATAGTGAAGAGCTAGATTAAGTCTCTTT 543
|||||
Db 301 GACACATATACCCGAGGAACTGCGCATGTATAGTGAAGAGCTAGATTAAGTCTCTTT 360
QY 544 CAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTCTGGACTCTAC 603
Db 361 CAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTCTGGACTCTAC 420
QY 604 TACACAGTATTGGTGACCAAGTGCAGTCTTTTGTGTGGTGGAACTGAAAAATTGG 663
Db 421 TACACAGTATTGGTGACCAAGTGCAGTCTTTTGTGTGGTGGAACTGAAAAATTGG 480
QY 664 GAACCTTGATGCGTGGCTGGTCAGACACAGGCGGACACTTTCCTAAATGCTTTGTT 723
Db 481 GAACCTTGATGCGTGGCTGGTCAGACACAGGCGGACACTTTCCTAAATGCTTTGTT 540
QY 724 TTGGGCGGAACTTTAATATTGCAAGTGAAT 754
Db 541 TTGGGCGGAACTTTAATATTGCAAGTGAAT 571

RESULT 3
BM459898 1041 bp mRNA linear EST 05-FEB-2002
AGENCY: NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5532247
5', mRNA sequence.
BM459898
BM459898.1 GI:18508938
EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12215 row: d column: 08
High quality sequence stop: 567.
FEATURES
source
1..1041
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5532247"
/clone_lib="NIH_MGC_71"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.1 kb."
BASE COUNT 297 a 208 c 266 g 269 t 1 others
ORIGIN
Query Match 10.8%; Score 567; DB 13; Length 1041;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 617; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGAGTGGACAGTCTCTTTTCAAGAGAGAGATGACTTTTAACAGTTTGAAGATCT 60
|||||
Db 34 GAAGAGTGGACAGTCTCTTTTCAAGAGAGAGATGACTTTTAACAGTTTGAAGATCT 93
```

```
QY 61 AAAACTTGTGTACCTGCAGACATCAATAGGAAGAAGAAATTTGTAGAAGAGTTTATAGA 120
|||||
Db 94 AAACTTGTGTACCTGCAGACATCAATAGGAAGAAGAAATTTGTAGAAGAGTTTATAGA 153
QY 121 TTAATAAATTTTGGTAAATTTTCCAAAGTGGTAGTCTCTTTTTCAGCATCAACACTGGCAGCA 180
Db 154 TTAATAAATTTTGGTAAATTTTCCAAAGTGGTAGTCTCTTTTTCAGCATCAACACTGGCAGCA 213
QY 181 GCAGGTTTCTTTTATCTACTGTTGAAGAGATACCGTCCGCTGCTTTTGTCTATGAGCT 240
Db 214 GCAGGTTTCTTTTATCTACTGTTGAAGAGATACCGTCCGCTGCTTTTGTCTATGAGCT 273
QY 241 GTAGATAGATGCAATATATGGAGACTCAGCAGTTTGAAGAGACACAGGAAAGTATCCCCAAAT 300
Db 274 GTAGATAGATGCAATATATGGAGACTCAGCAGTTTGAAGAGACACAGGAAAGTATCCCCAAAT 333
QY 301 TGCAGATTTATCAACGGCTTTTATCTTTGAAATAGTGCACCGAGTCTACAAATTCGTGT 360
Db 334 TGCAGATTTATCAACGGCTTTTATCTTTGAAATAGTGCACCGAGTCTACAAATTCGTGT 393
QY 361 ATCCAGAAATGCTCAGTACAAAGTTGAAACTATCTGGGAGCAGAGATCATTTTGCCTTA 420
Db 394 ATCCAGAAATGCTCAGTACAAAGTTGAAACTATCTGGGAGCAGAGATCATTTTGCCTTA 453
QY 421 GACAGGCCATCTGAGACACATGACGACTATCTTTTTCAGAACTGGGAGGTTGTAGATATA 480
Db 454 GACAGGCCATCTGAGACACATGACGACTATCTTTTTCAGAACTGGGAGGTTGTAGATATA 513
QY 481 TCAGACACCATATACCCGAGGAACTGCTGATATAGTGAAGAGCTAGATTAAGATCC 540
Db 514 TCAGACACCATATACCCGAGGAACTGCTGATATAGTGAAGAGCTAGATTAAGATCC 573
QY 541 TTTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGAGTTTACAAAGTCTGGACTC 600
Db 574 TTTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGAGTTTACAAAGTCTGGACTC 633
QY 601 TACTACACAGGTATTGTT 618
Db 634 TACTACACAGGTATTGTT 651

RESULT 4
AI628066/c
LOCUS
DEFINITION
similar to SW:IAF3_HUMAN P98170 INHIBITOR OF APOPTOSIS PROTEIN 3 ; ,
mRNA sequence.
ACCESSION AI628066
VERSION AI628066.1 GI:4664866
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 784)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor gene index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert length: 472 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 466
```

FEATURES	POLYA-No.		Location/Qualifiers		EST.	
	source	1..784	/organism="Homo sapiens"	/db_xref="taxon:9606"	human.	human.
			/clone="IMAGE:285739"	/lab_host="NCI_CGAP_Kid11"		
			/lab_host="DH10B"			
			/note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo."			
BASE COUNT		266 a	152 c	106 g	255 t	5 others
ORIGIN						
		Query Match 10.5%; Score 551; DB 9; Length 784;				
		Best Local Similarity 100.0%; Pred. No. 0;				
		Matches 551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1419	TGTTCCCTTGGGACATCTAGTCACCTTGTAAACAATGTGCTGAAGCAGTGGACAAGTGTC	1478			
Db	563	TGTTCCCTTGGGACATCTAGTCACCTTGTAAACAATGTGCTGAAGCAGTGGACAAGTGTC	504			
QY	1479	CATGTGCTACACAGTCATTAATCTCAAGCAAAAATTTTATGTCCTAACTTAACCTAT	1538			
Db	503	CATGTGCTACACAGTCATTAATCTCAAGCAAAAATTTTATGTCCTAACTTAACCTAT	444			
QY	1539	AGTAGGCATGTTATGTTGTTTATTACCTGATTTGAATGTGATGCTGAACCTGACTTTA	1598			
Db	443	AGTAGGCATGTTATGTTGTTTATTACCTGATTTGAATGTGATGCTGAACCTGACTTTA	384			
QY	1599	AGTAATCAGGATTGAATTCATTAGCATTTGCTACCAAGTAGGAAAAAATGTACATGG	1658			
Db	383	AGTAATCAGGATTGAATTCATTAGCATTTGCTACCAAGTAGGAAAAAATGTACATGG	324			
QY	1659	CAGTGTTTGTAGTGGCAATATATCTTGAATTTCTTGATTTTTCAGGGTATTAGCTGTA	1718			
Db	323	CAGTGTTTGTAGTGGCAATATATCTTGAATTTCTTGATTTTTCAGGGTATTAGCTGTA	264			
QY	1719	TTATCCATTTTCTTACTGTTATTATTTGAAACCATAGACTAAGATAAGAAGCATCAT	1778			
Db	263	TTATCCATTTTCTTACTGTTATTATTTGAAACCATAGACTAAGATAAGAAGCATCAT	204			
QY	1779	ACTATACTGAACACATGTATTCTCATAGTACTGATTTAATTTCTTAAGTGTAAAGTGA	1838			
Db	203	ACTATACTGAACACATGTATTCTCATAGTACTGATTTAATTTCTTAAGTGTAAAGTGA	144			
QY	1839	ATTAATCATCTGGATTTTATTTCTTTTTCAGATAGGCTTAACAAATGGAGCTTCTGTAT	1898			
Db	143	ATTAATCATCTGGATTTTATTTCTTTTTCAGATAGGCTTAACAAATGGAGCTTCTGTAT	84			
QY	1899	ATAAATGTGGAGATTAGAGTTAATCTCCCAATCACATATTTGTTGTGTAAGG	1958			
Db	83	ATAAATGTGGAGATTAGAGTTAATCTCCCAATCACATATTTGTTGTGTAAGG	24			
QY	1959	AATAAATTTGTT	1969			
Db	23	AATAAATTTGTT	13			
RESULT 5						
AL713196						
LOCUS						
DEFINITION		AL713196 529 bp mRNA linear EST 22-MAR-2002				
		DKFZp686M1895_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone				
		DKFZp686M1895 5', mRNA sequence.				
ACCESSION		AL713196				
VERSION		AL713196.1 GI:19696552				

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

EST.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 529)

Bloecker, H., Boecher, M., Brandt, P., Mewes, W., Weil, B. and Wiemann, S.

EST (Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Weil, B. and Wiemann, S.)

Unpublished (1999)

MIPS

Am Klopferspitz 18a D-82152 Martinsried, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.

No sl sequence available.

This clone (DKFZp686M1895) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers

1..529

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="DKFZp686M1895"

/clone\_lib="686 (synonym: hlcc3)"

/tissue\_type="human skeletal muscle"

/dev\_stage="adult"

/lab\_host="DH10B"

/note="Vector: pTriplex2; site\_1: sfIIA; site\_2: sfIIB; cDNA-collection"

BASE COUNT

165 a

96 c

126 g

142 t

ORIGIN

Query Match 9.0%; Score 469; DB 9; Length 529;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 469; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 GATGACCTTTTAACAGTTTGAAGGATCTAAACTTGTGTACCTGCAGACATCAATAAGGA 92

Db 61 GATGACCTTTTAACAGTTTGAAGGATCTAAACTTGTGTACCTGCAGACATCAATAAGGA 120

QY 93 AGAAGAATTTGTAGAGAGTTTAATAGATTAAAAACTTTTGCTAAATTTCCAAAGTGGTAG 152

Db 121 AGAAGAATTTGTAGAGAGTTTAATAGATTAAAAACTTTTGCTAAATTTCCAAAGTGGTAG 180

QY 153 TCCTGTTTCAGCATCAACACTGGCAGCAGAGGGTTTCTTTTATACTGGTGAAGGAGATAC 212

Db 181 TCCTGTTTCAGCATCAACACTGGCAGCAGAGGGTTTCTTTTATACTGGTGAAGGAGATAC 240

QY 213 CGRGGGTGCTTTAGTTGTCATGCTGATAGTAGTGGCAATATGGAGACTCAGCAGT 272

Db 241 CGRGGGTGCTTTAGTTGTCATGCTGATAGTAGTGGCAATATGGAGACTCAGCAGT 300

QY 273 TGAAGACACAGAGAAAGTATCCCCAAATTCAGATTATCAACGGCTTTTATCTTGAAGA 332

Db 301 TGAAGACACAGAGAAAGTATCCCCAAATTCAGATTATCAACGGCTTTTATCTTGAAGA 360

QY 333 TAGTGCACGCTGTACAAATTTCTGGTATCCAGAATGGTCAGTACAAAGTTGAAAACCTA 392

Db 361 TAGTGCACGCTGTACAAATTTCTGGTATCCAGAATGGTCAGTACAAAGTTGAAAACCTA 420

QY 393 TCTGGGAAGCAGAGATCATTTTGCCTTAGACAGGCCATCTGAGACACATCGACACTATCT 452

Db 421 TCTGGGAAGCAGAGATCATTTTGCCTTAGACAGGCCATCTGAGACACATCGACACTATCT 480

QY 453 TTTGAGAACTGGCGAGGTGCTAGATATATATATATATATATATATATATATATATATAT 501

Db 481 TTTGAGAACTGGCGAGGTGCTAGATATATATATATATATATATATATATATATATATATAT 529



sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCCGAGCGCGCATG-dT(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.85  
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."

BASE COUNT 147 a 81 g 216 t  
ORIGIN

Query Match 8.6%; Score 450; DB 12; Length 537;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4169 CTCCAACTCTTAATCAAAATTTTGGAGACTTAACAGCATTTGCTGTTGAACATATA 4228  
DB 1 CTCCAACTCTTAATCAAAATTTTGGAGACTTAACAGCATTTGCTGTTGAACATATA 60  
QY 4229 AAAGCACCAGGATCTTTCCATCTAATTCGCCAAATAATGATCATTTGCCAAGTCAAAACT 4288  
DB 61 AAAGCACCAGGATCTTTCCATCTAATTCGCCAAATAATGATCATTTGCCAAGTCAAAACT 120  
QY 4289 ATAGCCATATCCAAATCTTTTCCCTCCCAAGAGTCTCAGTGTCTACATGTAGACTAT 4348  
DB 121 ATAGCCATATCCAAATCTTTTCCCTCCCAAGAGTCTCAGTGTCTACATGTAGACTAT 180  
QY 4349 TCCTTTTCTGTATAAGTTTCACCTCTAGGATTTCAAGTCACCACCTATTTTACATTTTAGT 4408  
DB 181 TCCTTTTCTGTATAAGTTTCACCTCTAGGATTTCAAGTCACCACCTATTTTACATTTTAGT 240  
QY 4409 CATGCCAAGATTTCAAGTAGTTTTCGAATAGTACTTATCTTTATTTGTAATAATTTAGTC 4468  
DB 241 CATGCCAAGATTTCAAGTAGTTTTCGAATAGTACTTATCTTTATTTGTAATAATTTAGTC 300  
QY 4469 TGTGTATCAAAAGCATGCTTAATTTTGGAGACTGTTTTCAGTGTAGACTATTCACAACTAAAT 4528  
DB 301 TGTGTATCAAAAGCATGCTTAATTTTGGAGACTGTTTTCAGTGTAGACTATTCACAACTAAAT 360  
QY 4529 TCAGTGTAAATTAATAGCTTTATATTCCTTTCCTGCTACATTTGGTTTTTCCCTTCCCT 4588  
DB 361 TCAGTGTAAATTAATAGCTTTATATTCCTTTCCTGCTACATTTGGTTTTTCCCTTCCCT 420  
QY 4589 GTCCCTTTGATTACGGGCTAAGTAGGGTA 4618  
DB 421 GTCCCTTTGATTACGGGCTAAGTAGGGTA 450

RESULT 8  
BF510268/c  
LOCUS  
DEFINITION  
UI-H-BI4-api-d-01-0-UI.s1 NCI\_CGAP\_Sub8 Homo sapiens cDNA clone  
IMAGE:3087408 3', mRNA sequence.

ACCESSION  
BF510268  
VERSION  
BF510268.1 GI:11593566  
KEYWORDS  
EST.  
SOURCE  
human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 462)  
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapsb-re@mail.nih.gov](mailto:cgapsb-re@mail.nih.gov)

The sequence contained an oligo-dT track that was present in the  
oligonucleotide that was used to prime the synthesis of first  
strand cDNA and therefore this may represent a bonafide poly A  
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:  
NCI-CGAP clone distribution information can be found through the  
I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Seq primer: M13 Forward  
POLYA=yes.  
FEATURES  
Source  
Location/Qualifiers  
1..462  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="IMAGE:3087408"  
/clone\_lib="NCI\_CGAP\_Sub8"  
/lab\_host="DH10B (Life Technologies)"  
/note="Vector: pr773D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not 1; Site\_2: Eco RI; NCI\_CGAP\_Sub8  
is a subtracted library derived from NCI\_CGAP\_Sub5. The  
NCI\_CGAP\_Sub8 library had 2.5 million recombinants. A  
single-stranded DNA preparation of NCI\_CGAP\_Sub5 was used  
as a tracer in a subtractive hybridization with a driver  
comprising: a pool of clones from NCI\_CGAP\_Sub5 (IMAGE  
clone ids 2732833-2737415, 3068040-3069191; 25% of the  
driver population), a pool of clones from NCI\_CGAP\_Sub4  
(IMAGE clone ids 2723592-2729326; 25% of the driver  
population), NCI\_CGAP\_Sub6 (pool AIF-AJU, IMAGE ids  
2728969-2733190; 25% of the driver population), and  
NCI\_CGAP\_Sub7 (IMAGE ids 3069192-3072238, 3081864-3084550  
; 25% of the driver population). Subtraction was  
performed as previously described [Bonaldo, Lennon &  
Soares (1996): Normalization and Subtraction: Two  
Approaches To Facilitate Gene Discovery. Genome Research  
6, 791-806.  
TAG\_LIB=NCI\_CGAP\_Lu5  
TAG\_TISSUE=lung  
TAG\_SEQ=CAAC"

BASE COUNT 172 a 80 c 73 g 137 t  
ORIGIN

Query Match 8.3%; Score 434; DB 12; Length 462;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3725 CCTGTTCTCTGTTTATGATGTAATCCTCAGTTCTTTCACCTTTCGACTCTGCGCACTT 3784  
DB 445 CCTGTTCTCTGTTTATGATGTAATCCTCAGTTCTTTCACCTTTCGACTCTGCGCACTT 386  
QY 3785 AGTTTGGTTATATAGTCATTAACCTGAAATTTGGTCTGTATAGTCTAGACTTTAAATTTAA 3844  
DB 385 AGTTTGGTTATATAGTCATTAACCTGAAATTTGGTCTGTATAGTCTAGACTTTAAATTTAA 326  
QY 3845 AGTTTCTACAGGGGAGAAAGTGTAAATTTTAAATATGTTTTCAGGACACTTC 3904  
DB 325 AGTTTCTACAGGGGAGAAAGTGTAAATTTTAAATATGTTTTCAGGACACTTC 266  
QY 3905 ACTTCCAAGTCAGGTAGGTCAATCTAGTTGTTAGCCAAAGGACTCAAGGACTGAATTT 3964  
DB 265 ACTTCCAAGTCAGGTAGGTCAATCTAGTTGTTAGCCAAAGGACTCAAGGACTGAATTT 206  
QY 3965 GTTTTAAACATAAGGCTTTTCCTGTTCTGGAGCGGCACTTCATTAAATTTCTTCTAAAC 4024  
DB 205 GTTTTAAACATAAGGCTTTTCCTGTTCTGGAGCGGCACTTCATTAAATTTCTTCTAAAC 146  
QY 4025 TTGCTATGTTTAGAGTTAAGCAAGACTTTTCTTCTCTCCATGAGTCTGAAATTTAA 4084  
DB 145 TTGCTATGTTTAGAGTTAAGCAAGACTTTTCTTCTCTCCATGAGTCTGAAATTTAA 86  
QY 4085 TGCACACCGCTGATGGGCTAACCAAGTTTATTTTAAAGAAATGTTTGAATGCTGTGCT 4144  
DB 85 TGCACACCGCTGATGGGCTAACCAAGTTTATTTTAAAGAAATGTTTGAATGCTGTGCT 26  
QY 4145 TCAGGTTCTTAAAA 4158  
DB 25 TCAGGTTCTTAAAA 12

RESULT 9  
BG164322  
LOCUS  
BG164322 943 bp mRNA linear EST 06-FEB-2001

```

DEFINITION 602341372f1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4449280 5',
            mRNA sequence.
ACCESSION  BG164322
VERSION    BG164322.1  GI:12671025
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 943)
            NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS    National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE      Unpublished (1999)
JOURNAL
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LAM10232 row: p column: 17
            High quality sequence stop: 670.
FEATURES   source
            location/Qualifiers
            1..943
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:4449280"
            /clone_lib="NIH_MGC_89"
            /tissue_type="hybernephroma, cell line"
            /lab_host="DH10B (phage-resistant)"
            /note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
            Site_2: SalI; Cloned unidirectionally; oligo-dr primed.
            Average insert size 1.3 kb. Library enriched for
            full-length clones and constructed by Life Technologies.
            Note: this is a NIH_MGC Library."
BASE COUNT 297 a 144 c 185 g 317 t
ORIGIN
Query Match 8.3%; Score 432; DB 12; Length 943;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 602; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 3827 TCTAGACTTTAAATTAAGTTTCTACAGGGGAGAAAAGTGTTAAATTTTAAATA 3886
DB 1 TCTAGACTTTAAATTAAGTTTCTACAGGGGAGAAAAGTGTTAAATTTTAAATA 60
QY 3887 TGTTCCTCCAGGACACTTCACCTCCCAAGTCAGGTAGTTCACATCTAGTTGTTAGCCAA 3946
DB 61 TGTTCCTCCAGGACACTTCACCTCCCAAGTCAGGTAGTTCACATCTAGTTGTTAGCCAA 120
QY 3947 GGACTCAGGACTGAATGTTTAAACATAAGGCTTTTCTGTTCTGGGAGCGGCACTTCA 4006
DB 121 GGACTCAAGGACTGAATGTTTAAACATAAGGCTTTTCTGTTCTGGGAGCGGCACTTCA 180
QY 4007 TTAATAATCTCTTAAACTGTATCTTTAGAGTTTAAAGCAAGACTTTTCTCTCTCTCC 4066
DB 181 TTAATAATCTCTTAAACTGTATCTTTAGAGTTTAAAGCAAGACTTTTCTCTCTCTCC 240
QY 4067 ATGAGTTGTGAATTTAATGCACACGCTGTGTGGCTAACAAAGTTATTTTAAAGAAATG 4126
DB 241 ATGAGTTGTGAATTTAATGCACACGCTGTGTGGCTAACAAAGTTATTTTAAAGAAATG 300
QY 4127 TTTAGAAATGCTGTGCTTCAAGTTCTTTAAATCACTCAGCACTCCAATCTTAATCAAA 4186
DB 301 TTTAGAAATGCTGTGCTTCAAGTTCTTTAAATCACTCAGCACTCCAATCTTAATCAAA 360
QY 4187 TTTTGGAGACTTAACACGATTTGCTGTGTTGAACATATAAAAGACCGGATCTTTTC 4246
DB 361 -TTTGGAGACTTAACACGATTTGCTGTGTTGAACATATAAAAGACCGGATCTTTTC 419
QY 4247 CATCTAATTCGCAAAAATTTGATCATTTTTGCAAAAGTCAAAACTATAGCCATATCCAAATCT 4306

```

```

DB 420 CATCTAATTCGCAAAAATAGATCATTTGCAAAAGTCAAAACTATAGCCATATCCAAATCT 479
QY 4307 TTTTCCCTCCCAAGAGTTCTCAGTCTCTACAGTCTAGACATATTCCTTTCTGTATAAAGT 4366
DB 480 TTTTCCCTCCCAAGAGTTCTCAGTCTCTACAGTCTAGACATATTCCTTTCTGTATAAAGT 539
QY 4367 TCACCTCTAGGATTTCAAGTCACCACTATTTTACATTTTAGTCATGCAAGATTTCAAGTA 4426
DB 540 TCACCTCTAGGATTTCAAGTCACCACTATTTTACATTTTAGTCATGCAAGATTTCAAGTA 599
QY 4427 GTTT 4430
DB 600 GTTT 603

RESULT 10
AI277821/c
LOCUS
DEFINITION qm50e01.x1 Soares_placenta_8to9weeks_2NBHP8to9W Homo sapiens cDNA
            clone IMAGE:1893144 3', mRNA sequence.
ACCESSION AI277821
VERSION   AI277821.1  GI:3900089
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 472)
            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 2306 Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 438.
FEATURES   Location/Qualifiers
            1..472
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:1893144"
            /clone_lib="Soares_placenta_8to9weeks_2NBHP8to9W"
            /dev_stage="two placenta: one from 8 weeks and another
            from 9 weeks post conception"
            /lab_host="DH10B (ampicillin resistant)"
            /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
            modified polylinker; Site_1: NotI; Site_2: EcoRI; 1st
            strand cDNA was primed with a NotI - oligo(dT) primer [5'
            TGTTACCAATCTGAAGTCGCGGCGGATTTTTTTTTTTTTTTT 3'],
            double-stranded cDNA was size selected, ligated to EcoRI
            adapters (Pharmacia), digested with NotI and cloned into
            the NotI and EcoRI sites of a modified pT7T3 vector
            (Pharmacia). Library constructed by Bento Soares and
            M.Fatima Bonaldo."
BASE COUNT 179 a 83 c 59 g 151 t
ORIGIN
Query Match 8.1%; Score 422; DB 9; Length 472;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1540 GTAGGCATGTTATGTTGTTCTTTATACCTGATTTGAATGATGTGATGTAAGTAA 1599
DB 454 GTAGGCATGTTATGTTGTTCTTTATACCTGATTTGAATGATGTGATGTAAGTAA 395
QY 1600 GTAATCAGGATTTGAATTTCCATTTAGCATTTGCTTACCAAGTAGGAAAAAATGTACATGGC 1659
DB 394 GTAATCAGGATTTGAATTTCCATTTAGCATTTGCTTACCAAGTAGGAAAAAATGTACATGGC 335

```



```
QY 1660 AGTGTCTTGGCAATATAATCTTTGAATTTCTTGATTTTTCAGGGTATTAGCTGTAT 1719
Db 334 AGTGTCTTGGCAATATAATCTTTGAATTTCTTGATTTTTCAGGGTATTAGCTGTAT 275
QY 1720 TATCCATTTTCTTACTGTATTATTAATCGAAACCATAGACTAAGATAAGAACATCATA 1779
Db 274 TATCCATTTTCTTACTGTATTATTAATCGAAACCATAGACTAAGATAAGAACATCATA 215
QY 1780 CTATACTGAACACAATGTCTATTCTATAGTATATCTGATTTAAATTTCTTAAGTGTAAAGTAA 1839
Db 214 CTATACTGAACACAATGTCTATTCTATAGTATATCTGATTTAAATTTCTTAAGTGTAAAGTAA 155
QY 1840 TTAATCATCTGGATTTTATTTCTTTTCAGATAGGCTTAAACAAATGGAGTTTCTGTATA 1899
Db 154 TTAATCATCTGGATTTTATTTCTTTTCAGATAGGCTTAAACAAATGGAGTTTCTGTATA 95
QY 1900 TAAATGTGGAGATTACAGTTAACTCCCAATCACATAATTTGTTGTGGAAGAAGGA 1959
Db 94 TAAATGTGGAGATTACAGTTAACTCCCAATCACATAATTTGTTGTGGAAGAAGGA 35
QY 1960 AT 1961
Db 34 AT 33

RESULT 11
AI299965/c
LOCUS
DEFINITION Q024a11.x1 NCI_CGAP_Lu5 406 bp mRNA linear EST 01-FEB-1999
IMAGE:1909436 3',
mRNA sequence.
ACCESSION AI299965
VERSION AI299965.1 GI:3959311
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 406)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbbrp/image/image.html
Insert Length: 491 Std Error: 0.00
Seq primer: -40UP from Gibco.
Location/Qualifiers
1. .406
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1909436"
/clone_lib="NCI_CGAP_Lu5"
/tissue_type="carcinoid"
/lab_host="DH10B"
/notes="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
neuroendocrine lung carcinoid, and was then primed with a
Not I - oligo(dT) primer. Double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT73 vector. Library is normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 153 a 74 c 66 g 113 t
ORIGIN
```

```
Query Match 7.8%; Score 406; DB 9; Length 406;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3745 GTAATCCCTCAGTCTTCACCTTTGCACCTGCTGCCACTTAGTTGGTTATATAGTCATT 3804
Db 406 GTAATCCCTCAGTCTTCACCTTTGCACCTGCTGCCACTTAGTTGGTTATATAGTCATT 347
QY 3805 AACTTGAATTTGGTCTGTATAGTCTAGACTTTAAATTTAAAGTTTCTCAAGGGGAGAA 3864
Db 346 AACTTGAATTTGGTCTGTATAGTCTAGACTTTAAATTTAAAGTTTCTCAAGGGGAGAA 287
QY 3865 AAGTGTAAATTTTAAATATATGTTTCCAGGACACTTCACTTCCAAAGTCAGGTAGGTA 3924
Db 286 AAGTGTAAATTTTAAATATATGTTTCCAGGACACTTCACTTCCAAAGTCAGGTAGGTA 227
QY 3925 GTTCAATCTAGTTGTTAGCCAAAGGACTCAGGACTGAAATTTGTTTAAACATAAGGCTTTTC 3984
Db 226 GTTCAATCTAGTTGTTAGCCAAAGGACTCAGGACTGAAATTTGTTTAAACATAAGGCTTTTC 167
QY 3985 CTGTTCTGGAGCGGCACCTTCATTAATAATCTCTTAAACTTCTATGTTTAAAGTTTAAAGC 4044
Db 166 CTGTTCTGGAGCGGCACCTTCATTAATAATCTCTTAAACTTCTATGTTTAAAGTTTAAAGC 107
QY 4045 AAGACTTTTTTCTCTCCATGAGTTGTGAAATTTAAATGCAACGCTGATGGCT 4104
Db 106 AAGACTTTTTTCTCTCCATGAGTTGTGAAATTTAAATGCAACGCTGATGGCT 47
QY 4105 ACAAGTTTATTTAGAATTTTGAATGCTGTTGCTTCAGGT 4150
Db 46 ACAAGTTTATTTAGAATTTGTTTGAATGCTGTTGCTTCAGGT 1

RESULT 12
AW665401/c
LOCUS
DEFINITION hi90c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2979566 3', mRNA sequence.
ACCESSION AW665401
VERSION AW665401.1 GI:7457948
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 508)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 464.
Location/Qualifiers
1. .508
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2979566"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/notes="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBH19W, testis NHT, and B-cell
NCI-CGAP GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 6826332-687239,
```



Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation by: M. Bento Soares, Ph.D.  
DNA Library Arrayed by: Greg Lennon, Ph.D.  
National Institutes of Health, Mammalian Gene Sequencing Center  
Cloned distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Insert Length: 489 Std Error: 0.00  
Seq primer: -40UP from Gibco.

FEATURES  
source  
1. .413  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2272744"  
/clone\_lib="NCI CGAP Lu24"  
/tissue\_type="carcinoid"  
/lab\_host="DH10B"

/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 154 a 76 c 67 g 116 t  
ORIGIN  
Query Match 7.6%; Score 398; DB 9; Length 413;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3743 ATGTAATCCTCAGTCTTCACCTTTGCCACTGCTGCCACTAGTTGGTATATAGTCA 3802  
Db 413 ATGTAATCCTCAGTCTTCACCTTTGCCACTGCTGCCACTAGTTGGTATATAGTCA 354  
QY 3803 TTAACCTGAATTTGGTCTGTATAGTCTAGACCTTTAAAGTTTCTTACAAAGGGGAG 3862  
Db 353 TTAACCTGAATTTGGTCTGTATAGTCTAGACCTTTAAAGTTTCTTACAAAGGGGAG 294  
QY 3863 AAAAGTGTTAAATTTTAAATATATTTTCCAGGACACTTCACTTCCAAAGTCAGTAGG 3922  
Db 293 AAAAGTGTTAAATTTTAAATATATTTTCCAGGACACTTCACTTCCAAAGTCAGTAGG 234  
QY 3923 TAGTCAATCTAGTCTTACGCAAGCACTCAAGGACTGAATGCTTTTAAACATAAGGCTTT 3982  
Db 233 TAGTCAATCTAGTCTTACGCAAGCACTCAAGGACTGAATGCTTTTAAACATAAGGCTTT 174  
QY 3983 TCCTGTTCTGGGAGCGGCACCTTCATTAAAAATCTTCTTAAACACTTGTATGTTAGACTTAA 4042  
Db 173 TCCTGTTCTGGGAGCGGCACCTTCATTAAAAATCTTCTTAAACACTTGTATGTTAGACTTAA 114  
QY 4043 GCAAGACTTTTTTCTTCCCTCCATGAGTGTGAAATTTAATGCAACACGCTGATGTGG 4102  
Db 113 GCAAGACTTTTTTCTTCCCTCCATGAGTGTGAAATTTAATGCAACACGCTGATGTGG 54  
QY 4103 CTAACAAGTTTATTTTAAAGAAATGTTTAAAGTGTCT 4140  
Db 53 CTAACAAGTTTATTTTAAAGAAATGTTTAAAGTGTCT 16

RESULT 15  
BI823020  
LOCUS 603039619F1 NIH\_MGC\_115 Homo sapiens cDNA clone IMAGE:5180525 5',  
DEFINITION mRNA sequence.  
ACCESSION BI823020  
VERSION BI823020.1 GI:15934570  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

\* : \* \*

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 707)  
NIH-MGC http://mgs.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM11450 row: e column: 06  
High quality sequence stop: 565.  
Location/Qualifiers  
1. .707  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5180525"  
/clone\_lib="NIH\_MGC\_115"  
/lab\_host="DH10B"

/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH\_MGC Library."

BASE COUNT 204 a 105 c 146 g 252 t  
ORIGIN  
Query Match 7.4%; Score 389; DB 13; Length 707;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 439; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2096 TTTTGAAGCGTATTAAATGATAGTAATCTATCGAGCCCAACATGTGACATGGAAGA 2155  
Db 109 TTTTGAAGCGTATTAAATGATAGTAATCTATCGAGCCCAACATGTGACATGGAAGA 168  
QY 2156 TGTCAAAGATATGTTAAGTGTAAATGCAAGTGGCAAAACACTATGTATAGTCTGAGCCA 2215  
Db 169 TGTCAAAGATATGTTAAGTGTAAATGCAAGTGGCAAAACACTATGTATAGTCTGAGCCA 228  
QY 2216 GATCAAAGTATGTATGTTTTTAAATATGATAGCAACAAAGATTGGAAAGATATACCCA 2275  
Db 229 GATCAAAGTATGTATGTTTTTAAATATGATAGCAACAAAGATTGGAAAGATATACCCA 288  
QY 2276 AACTGTTAAATGGGTTCTCTTCGGGGAGGGGGGATGGGGAGGGGGCCCCAGAGGGG 2335  
Db 289 AACTGTTAAATGGGTTCTCTTCGGGGAGGGGGGATGGGGAGGGGGCCCCAGAGGGG 348  
QY 2336 TTTTATAGGGGCTTTTCACTTTCTACTTTTTCATTTTGTCTGTCGAAATTTTATA 2395  
Db 349 TTTTATAGGGGCTTTTCACTTTCTACTTTTTCATTTTGTCTGTCGAAATTTTATA 408  
QY 2396 AGTATGTTACTTTTGTAAATCAGAAATTTTGAAGAGTATTTTGTGATTTAAAGCTTA 2455  
Db 409 AGTATGTTACTTTTGTAAATCAGAAATTTTGAAGAGTATTTTGTGATTTAAAGCTTA 468  
QY 2456 GGCATGTTCAACGCTCGAAACACTACTTATCTACGCTTAGTGTTCCTAATCAAGA 2515  
Db 469 GGCATGTTCAACGCTCGAAACACTACTTATCTACGCTTAGTGTTCCTAATCAAGA 528  
QY 2516 AGGAGGGCAGTTAACTTTT 2535  
Db 529 AGGAGGGCAGTTAACTTTT 548

Search completed: November 10, 2002, 01:30:31  
Job time : 6614 secs

